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September 14, 2004, 15:03:35; Search time 13362 Seconds (without alignments) 6967.582 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-09-813-329-5 2148 1 ggcacgaggcgaacggacgt.....aaaaaaaaaaaaaactcgag 2148 Title: Perfect score: Sequence:

3470272 segs, 21671516995 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

6940544 Total number of hits satisfying chosen parameters:

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GenEmbl:* Database

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GIGLVVALLALTINGTTRVSHLDKELKSLKRYVDNLQQRLGINYLDFDEFQREYEN

ALI DYPKKVDGLTDEEDDDGDGLDSIADBEDDDVSYSSVDDVGADYEDYTDMLNKLN

NAHTGTTPTSETTAGEGEETDGASSAGNDDNVPDDFTSYNAHKKKQERKSRSIADVRN

BEQNI OGNHTELQEKSSNEATSKERPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHF

SHDQNGFI TYGQDTPALLOLOLNTVPTNNPHKVHTCHTSGLITVTNTGLYYVAQICYNN

AVLREGNNRSYPGIFKV"
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George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S. Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
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                                                                                          Submitted (15-NOV-2002) Berkeley Drosophila Lawrence Berkeley National Laboratory, One C Berkeley, CA 94720, USA. Sequence submitted by:
Berkeley Drosophila Genome Project
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Berkeley, CA 94720
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/product="RH51659p"
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/db_xref="G1:25013018"
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
1. _2152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cdna@fruitfly.berkeley.edu.
Location/Qualifiers
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/note="Longest ORF"
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/product="1246.2910.1"
/db_xref="121:2746.2910.1"
/db_xref="121:2910.1"
/db_xref="121:2910.
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Direct Submission
Submitted (10-MAY-1999) Department of Pathology, Comprehensive
Cancer Center, 1500 E. Medical Center Dr., Ann Arbor, MI 48109,
Location/Qualifiers
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llarity 100.0%; Pred. No. 0;
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

1 (bases 1 to 2101)
Inohara,N. and Nunez,G.
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Unpublished
2 (bases 1 to 2101)
Inohara, N. and Nunez, G.
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ORIGIN Query Match Best Local Similarity 98.7%; Score 2076.4; DB 3; Length 2159; Matches 2121; Conservative 0; Mismatches 6; Indels 21; Gaps 2; Oy 5 GGGGGGGGGTTTAAAGTGAAAAAGAAACGGTAAATCAGAGATCCCAAGCAAG	65 CGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCCGTTTCAGTTAACTACTACCAAG 124	GTTGTGTTTTTTTTTTTTTTTGGTTTTCGCTGTGCCTTTATCGCAACAGAACTGAT [GCGGAAGAGAAAACAAGCAGTAGACAAACAAGCGCGGTIILLTIGGCGAATGCGGAAGAAAACAAGAGTAGAAAACAAAACA	372 ¢CATCAGCAGCCCGAGGGTTTATCTATATAGATGTCGCAGCTTATCATCTCATGCTGTC 431 425 TGTGAGGTTGTTGTGTGCTCGTGTAGTATCTTAAATACATAGAGTGTGTTCATATAAA 484 11111111111111111111111111111111111		2 TCATCATCATCATCGTCGTCGTCATATCAACAGAATCAGCATCAGCATCTGGAGGCCCCGGT 5 TGCTCTAAGATCCCCCAGTGTTCATCAATTATGACTGCCGAGACCCTCCAAGCCGTTTATAA	665 CGCCAACGAGGCCAACGATGTTTTCCGGCCAAGGGACCAGCAGCGCCC 724 [1	TIGCCATTCTCGCACTAACGATCTGGCAGACACGCCTGTATCGCATCTGGACAAGGAGC	ACGAGTTCGACGAGTCCAAAAGGAGTACGAGGAGTGCCTCATCGACAAAACAAAC

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Igaki,T.

Direct Submission

Birect Submission

BIREN, Laboratory for Cell Recovery Mechanisms; 2-1 Hirosawa, Wako, Saitama 351-0198, Japan (E-mail:igaki@brain.riken.go.jp,

Tel:81-48-467-6945, Fax:81-48-467-6946)
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Aigaki,T. and Miura,M.
Eiger, a TNF superfamily ligand that triggers the Drosophila
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                                                                                                                                                                                        domain"
                                                                                                                                                                                                                                                                                                                                          Score 1202; DB 3;
Pred. No. 1.6e-263;
); Mismatches 0;
                                                                                                                                                                                        transmembrane
                                                                                                                                                                                                                                                      433. .438
/gene="darth"
/note="cleavage site"
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/gene="darth"
/note="Region: t
178. .1245
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0
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/note="Region:
                                                                                                                                                                                                                                                                                                                                           56.0%;
98.6%;
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Best Local Similarity 98.6
Matches 1230; Conservative
                                                                                                      misc_feature
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| translation="WITHETILEFFITPTSANDDGFPAKATSTATAQRETRQLIPLVLGF
| IGLGLVVAILALTIWQTTRVSHLDKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYEN
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GATAACGAGAGAAACTCTTATCAGGGACACTTTCAAACGCGCGATGGCGTCTTGACGGTG
                                                                                                                                        ACCAATACAGGCCTATATTACGTATACGCCCAGATATGCTACAACAACACCCACAG
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
BNoptera; Edopoterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organisma-Drosophila melanogaster"
/mol_type="mRNA"
/db xref="taxon:7227"
/chromosome="2"
/map="2R"
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Center, 5323 Harry Hines Blvd., Dallas, TX
Location/Qualifiers
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/gene="darth"
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/gene="darth"
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Chaudhary, P.M.
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/gene="CG12919"

/note="Longest ORF"

/codon start=1

/product="SD18286p"

/product="SD18286p"

/product="AAM51093.1"

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/db xref="G1:2143090"

/db xref=
     For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCAGAATATTCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACT 1350
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                                                                                                                                                                                                                      melanogaster"
                                                                                                                                                                                                                                                                                                   1. .1221
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170. .955
                                                                                                                                                                                                                organism="Drosophila
                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:7227"
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FILODA.

Drosophila melanogaster (fruit fly)

Evaluation melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Rooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Buydroidea; Drosophilidae; Drosophila;

Ephydroidea; Drosophilidae; Drosophila;

Stapleton,M., Brokerein,P., Hong,L., Agbayani,A., Carlson,J.,

Champe,M., Chavez,C., Dorsett,V., Dresnek,D., Farfan,D., Frise,E.,

George,R., Gonzalez,M., Guarin,H., Kronmiller,B., Li,P., Liao,G.,

Miranda,A., Mungall,C.J., Nunoo,J., Parleb,J., Paragas,V., Park,S.,

Patel,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Rubin,G.M.
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Direct Submission.

Submitted (07-JUN-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley Wational Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the geneme. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of CDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contominating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAS, and
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1 AC005974 AC005435 AC005436 AC005469
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Prosophila melanogaster (fruit fly)
                               Score 798.8; DB 2;
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, *** SEQUENCING IN PROGRESS ***.
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HTG; HTGS PHASE2.

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Nooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 55359)
Adams, M. and Venter, J.C.
Direct Submission
Submisted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
GGCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCAGATATGCTACAAC
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For further information on this sequence you may e-mail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   available
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This sequence will be replaced
by the finished sequence as soon as it is
the accession number will be preserved.
Location/Qualifiers
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/organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
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Drosophila melanogaster,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Deoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.

1 (bases 1 to 158983)

2 (clniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Cieiolak,L., Doyle,C.M., Farfan,D.E., Champe,M., Chavez,C., Chew,M., Caraney,L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomctan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Feiffer,B., Poon,L., Punch,E., Seduára,A., Sethi,H., Snir,E., Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R., Zleran,L.L. and Rubin,G.M. Sequencing of Drosophila chromosome 2R, region 46El-46F6

Libbses 1 to 158983)

Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,R.N.L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,R.N.L., Hoskins,R.A., Houston,R.A., Houston,M.A., Mazda,P., Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P., Feiffer,B., Poon,L., Punch,E., Requeira,A., Sethi,H., Snir,E., Sieran,L.L. and Rubin,G.M.

Svirskas,R.R., Twomey,B., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.

Submitted (19-NoV-1988) Berkeley Drosophila Genome Project, MS etheley, CA 94720, US
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/note="These Pls were completed as a project. DS05181
[D384] is a partial bridge with list distal neighbor
extending from pl to Pl end at bp 57,624. DS01913 (D350)
extends from Pl end at 7,924 to Pl end at 92,484. DS05033
(D347) extends from Pl end at bp 60,881 to Pl end at bp
158,983. Between bps 53,139 and 53,140, Th10 was excised
from DS05181 along with an associated 9 bp duplication."
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/Clone="Pls DS05033 (D347), DS01913 (D350), and DS05181
(D384)"
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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/db xref="taxon:7227"
/chromosome="2R"
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Best Local Similarity 99.8
Matches 800; Conservative
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Loughina melanogater intur 117,

Drosophila melanogater

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Booptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

S Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,

Rogers, Y., An, H., Baldwin, D., Banzon, J., Besson, K.Y., Busam, D.A.,

Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,

Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,

Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,

Gorzalez, M. Houck, J. Hoskins, R.A., Hostin, D., Howland, T.J.,

Ibegwam, C., Jalali, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,

Pacleb, J., Paragas, V., Park, S., Patel, S., Scheeler, F.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
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2 (bases 1 to 189620)

3S Calniker'S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
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Ferriera, S., Frise, E. (Galle, R.F., Garg, N.S., George, R.A.,
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Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
McIntosh, T.C., May, M., Wurphy, B., Walson, C., Nelson, K.A., Nunoo, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
Shouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
Direct Submission

AL Submitted (08-NOV-2001) Berkeley Drosophila Genome Project, MS
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Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilae; Drosophila.

Ephydroidea; Drosophilae; Drosophila.

Ecanisco, Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

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Ferriacra, S., Frise, E. (Galle, R.F., Garg, N.S., George, R.A.,

Incompact, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

Incompact, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Monoo, J.,

Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Zaveri, J.S., Smitch, H.O., Rubin, G. M. and Venter, J.C.

Sequencing, of Drosophila chromosome 2R, region 460-47A
133826 TGCTCTAAGATCCCCCAGTGTTCATCAATTATGACTGCCGAGACCCTCAAGCCGTTTATAA 133885
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                        L Submitted (18-ARP-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Sep 6, 2010 this sequence version replaced gi:13324748.

Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence)) or send email to bdgp@fruitfly.berkeley.edu.
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                                                                                          Blazej, R.G.,
                        Unpublished

Loades 1 to 179904)

Claiker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacheb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Syirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
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   Sequencing of Drosophila chromosome 2R, region 46C-46D
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Pred. No. 8.1e-171;
0; Mismatches 2;
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Science 287 (5461), 2185-2195 (2000)
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Drosophila melanogaster chromosome
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This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.

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   Berkeley National Laboratory, One Cyclotron Road,
0, US
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64-121, Lawrence Berkeley National Laboratory, Or
Berkeley, CA 94720, US
Sequency Drosophila Genome Project
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
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Pred. No. 8.3e-171;
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ISM Drosophila melanogaster (fruit fly)

Brosophila melanogaster

Bukaryota; Merazaa; Arthropoda; Haxapoda; Insecta; Pterygota; Brosophila melanogaster

Bukaryota; Merazaa; Arthropoda; Brachyeera; Muscomorpha;

CE 1 (Dases 1 to 27530)

RS Adama, D., Celniker, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., Garle, C., Scherrs, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., Gutcon, G.G., Morrman, J.Y., Yandell, M.D., Zahang, Q., Chen, L.X., Manatides, P.G., Eaxer, E.G., Helle, G., Malson, C.R., Gabor, G.L., Marit, Doyle, C., Baxer, E.G., Helle, G., Malson, C., Baldwin, D. Baladon, N. W., Banos, P.W., Baras, B. B., Baradon, R. C., Rogers, Y.H., Blazel, R.G., Bayrakterser, Flankoch, C., Baldwin, D. Benson, K. Y., Benos, P.W., Berman, B. P. Bhandari, D., Bolshakov, S. Bortchan, M. M., Baru, A., Bard, R.C., Davenport, L.B., Burtis, K.C., Bussm, D.A., Buller, H., Doyle, D., Brottier, P., Denger, A., Denger, A., Denger, S., Davenport, L.B., Davengort, L.B., Davengort, B.C., Dunkov, B.C
                                             168792 AGGACGACCCAGCTGATCCCCCTGGTTTTGGGGTTCATCGGCTTGGGGCTGGTCG 168733
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Celniker,S.B., Adams,M.D., Kronmiller,B., Wan,K.H., Holt,R.A.,
Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y.,
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SNTLGGVLRCHTRGVWSVRFSPVDQIVLTSSSDCTLRIWSISNFSCIRRFDQECTILR
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                   4KVWQLVRSKEDRNSYSFNLRYAALSHDKBVNCVAYAPNNKLIATASQDKTAKVWLAE
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complement (join(44. 3521,3590. 4619,4684. .5341,5819. .5866,6647. .8156,8220. .8346,8412. .8546))
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                                                                                                                                                                                                                                    complement(2844. .13679)
/genne="BcDNA:GH06448"
/locus tags="CG1516"
/notes="last curated on Tue Mar 12 18:58:27 PST 2002"
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/product="CG1516" |
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/db_xref="FLYBASE:FB900027580" |
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5819. :5866,6647 | :8156,8220 | :8346,12506 | :12893) |
/gene="BcDNN:G1616348" |
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/product="CG1516" |
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complement {join(2844. .3521,3590. .4619,4684. .5341,
647. .8156,48220. .8544)}
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/gene="BCDNA:GH06348"
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Pred. No. 9.3e-171;
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Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwan, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Melson, C., Nelson, K.A., Nunco, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D., Williams, S.M., Zaveri, J.S., Smith, H.O., Venter, J.C. and Rubin, G.M., Sequencing of Drosophila melanogaster genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (23-JAM-2003) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
On Jul 1, 2002 this sequence version replaced gi:10727672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (06-SEP-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
6 (bases 1 to 275390)
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WQLDTGKLVKLWKAQHKGPVIRVEFSPCGRLICTSGGADATLRLWDYSNNSCLGALKD
                                                                                                                                                                                                                                                                                                                                                                                                                                             "(bases 1 to 275390)
Misra,S., Crosby,M.A., Matthews,B.B., Bayraktaroglu,L.,
Campbell,K., Hradecky,P., Huang,Y., Kaminker,J.S., Prochnik,S.E.,
Smith,C.D., Tupy,J.L., Bergman,C.M., Berman,B.P., Carlson,J.W.,
Celniker,S.E., Clamp,M.E., Drysdale,R.A., Emmert,D., Frise,E., de
Grey,A.D.N.J., Harris,N.L., Kronmiller,B., Marshall,B.,
Milburn,G.H., Richter,J., Russe,S., Searle,S.M.J., Smith,E.,
Shu,S., Smutniak,F., Whitfield,E.J., Ashburner,M., Gelbart,W.M.,
Rubin,G.M., Mungall,C.J. and Lewis,S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 275390)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
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\note="last curated on Mon Peb 11 17:53:43 PST 2002"
\map="46B7-46B9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
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       Kimura, M., Seki, N., Kimura, I., Yamada, S.
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                                                                                                                                            2 (bases 1 to 2040)
Takeuchi, K., Yamashita, S. and Yamada, S.
Direct Submission
Submitted (14-AUG-2003) Kazuharu Takeuchi, Nippon Suisan Kaisha,
Ltd., Central Research Laboratory; Kitanomachi, Hachioji, Tokyo
192-0906, Japan (E-mail: k-takeuchi@missui.co.jp,
Tel:81-426-56-5195, Fax:81-426-56-5188)
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                    and Yamashita,S.
Aspolin, a Novel Extremely Aspartic Acid-rich Protein in Fish
Muscle, Promotes Iron-mediated Demethylation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    899 ATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCGACTATCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="aspolin2"

/codon start=1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.1%; Score 67.2; DB 5; Length 2040;
llarity 50.6%; Pred. No. 0.00031;
Conservative 0; Mismatches 158; Indels 0.
                                                                                                                                                                                                                                                                                                      /organism="Theragra chalcogramma"
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/country="Japan: Hokkaido, Hakodate"
                                                                       Trimethylamine-N-oxide
J. Biol. Chem. 278 (48), 47416-47422 (2003)
22995865
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     Takeuchi, K., Hatanaka, A.,
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/gene="aspolin2"
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mRNA for aspartic acid-rich protein
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Theragra chalcogramma

Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii, Neopterygii; Teleostei; Euteleostei;

Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Theragra.
                                        64
                                                                                                                           CGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCCGTTTCAGTTAACTACTTACCAAG
                                                                                                                                                                           ATTGAATTTCGCCATCGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACTGTGT
                                                                                                                                                                                                     230639 ATTGAATTTCGCCATCGGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACTGTGT
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AB117518.1 GI:35210493
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1008 TCTGGATTCCATTGCGGACGACGACGACGACGTTAGCTATAGCTCTGTGGATGATGT 1067
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Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
Plant genes involved in defense against pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tracheophyta;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                    1 (bases 1 to 390)
Gold,Lu, Tuerk,C., Pribnow,D. and Smith,J.Drew.
Systematic polypeptide evolution by reverse translation
Patent: US 6194550-A 7 27-PEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 390;
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Pred. No. 0.00024;
0; Mismatches 187; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
/wol_type="unassigned DNA"
                                                                                                          Sequence 7 from patent US 6194550. AR135147
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                  ACGATGATGATGACGATGAC 880
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Similarity 48.9%;
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                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Theragra.
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                                                                                                                                                                       Takeuchi, K., Hatanaka, A., Kimura, M., Seki, N., Kimura, I., Yamada, S.
                                                                                                                                                                                                                                                                                                                      Takeuchi, K., Yamashita, S. and Yamada, S.
Takeuchi, K., Yamashita, S. and Yamada, S.
Direct Submission
Submitted (14-MUG-2003) Kazuharu Takeuchi, Nippon Suisan Kaisha,
Ltd., Central Research Laboratory, Kitanomachi, Hachioji, Tokyo
192-0906, Japan (E-mail:k-takeuchi@nissui.co.jp,
Tel:81-426-56-5195, Fax:81-426-56-5188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  621 ATGAAGATGATGATGACGACGATGATGATGATGACGATGATGATGATGATGATGACGACG
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                                                                                                                                                                                         and Yamashita,S.
Aspolin, a Novel Extremely Aspartic Acid-rich Protein in Fish
Muscle, Promotes Iron-mediated Demethylation of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Theragra chalcogramma"
/mol_type="mcNA"
/db_xref="taxon:48550"
/tisaue_type="skeletal muscle"
/country="Japan:Hokkaido, Hakodate"
                                                                                                                                                                                                                                                 Trimethylamine-N-oxide
J. Biol. Chem. 278 (48), 47416-47422 (2003)
22995865
                                                    Theragra chalcogramma (Alaska pollock)
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/gene="aspolin1"
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/gene="aspolin1"
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                  AB117517.1 GI:35210491
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                                                                          Theragra chalcogramma
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1610 TATA 1613 905 TCWW 908 ò qq

00:00 Search completed: September 15, 2004, Job time : 13370 secs

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RESULT 1
                                                                                          September 14, 2004, 14:52:20 ; Search time 1222 Seconds (without alignments) 7467.373 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
                                                                - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	116	Abk11678 DNA encod	Abk11679 DNA encod	Abl21473 Drosophil	Abl21472 Drosophil	Aaq21833 Randomisi		Aaf76910 Sequence	Aai72775 Oligo #7	Ada71938 Rice gene	Aaa30290 Kaposi's	Aaf82901 Nucleotid	Aba93487 Kaposi's	Aav73805 KSHV LUR	Aav19941 KSHV long	Abl32510 Human imm	Abz23375 Reverse c	Abz23374 Nucleotid	Abl06114 Drosophil	Abz42562 Human C-C	Aaa27006 Human cDN		Abq54407 Human ova
SUMMARIES	CI CI	ABK11680	ABK11678	ABK11679	ABL21473	ABL21472	AAQ21833	AAQ36859	AAF76910	AAI72775	ADA71938	AAA30290	AAF82901	ABA93487	AAV73805	AAV19941	ABL32510	ABZ23375	ABZ23374	ABL06114	ABZ42562	AAA27006	ABV57409	ABQ54407
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ACH22127	ABL3331	AA18757	ABV56603	ABL0331	ABL0331	ACH43937	AAA26447	ADA56	ADC73	ADD37	AAH35025	ABX41	AAI87	AAT72	ABV60	AAH71	ABL33958	ABX49	AA143436	ACF35	AAS01
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ALIGNMENTS

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Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder; sparse hair; sweat gland aberration; endotoxic shock; inflammation; haemorrhagic necrosis of tumour; cytotoxicity; TNFv2; obesity-linked insulin resistance; gene; ds.
                                                                                                                                                                                                                                                       /notes "Tumour necrosis factor variant 1" 634...1860 /*tag= d /notes "Specifically claimed in claim 22" 634...789
                                                                   DNA encoding tumour necrosis factor variant 2 (TNFv2).
                                                                                                                                                                                                                                                                                                                                           /*tag= c
/label= mature_TNFv1
                                                                                                                                                                                                          Location/Qualifiers
634. .1863
                                                                                                                                                                                                                                  /*tag= b
/product= "TNFv1"
BP.
ABK11680 standard; DNA; 2148
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                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-2001; 2001US-00813329.
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790. .1860
                                            (first entry)
                                                                                                                                                                                    Drosophila melanogaster.
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(CHEN/) CHEN J.
(RAMA/) RAMANATHAN C S.
(XIAO/) XIAO H.
                                                                                                                                                                                                                                                                                                                                                                              US2002012968-A1.
                                                                                                                                                                                                                                                                      misc_difference
                                            05-JUN-2002
                                                                                                                                                                                                                                                                                                        sig_peptide
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                                                                                                                                                                                                                                                                                                                                mat_peptide
                      ABK11680;
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us-09-813-329-5.rng

Bowen MA;

Guan B,

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Page

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New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm animals.
                          Xiao
                          Ramanathan CS,
                                                                                                      Claim 2; Fig 3A-C; 119pp; English.
                       Carroll PM, Chen J,
                                       WPI; 2002-195121/25
(GUAN/) GUAN B.
(BOWE/) BOWEN M A.
                                                P-PSDB; AAU77718
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The invention describes an isolated tumour necrosis factor polypeptide (TMF). The polypeptide and polymucleotide are useful in controlling agriculturally important peets, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polymucleotide are useful for modulating the polymeptide and polymucleotide may be useful for modulating the polymeptide and polymucleotide may be useful for treating. Thus ameliorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorders, e.g. sparse hair, abnormal or missing teeth or sweat gland aberrations in animals (e.g. insects and potentially humans), condotxic shock, inflammation, haemorrhagic necrosis of tumours, cytotoxicity and obesity-linked insulin resistance, all of which involve necrosis factor variant 2 (TNFv2) protein, described in the invention

Sequence 2148 BP; 645 A; 510 C; 506 G; 487 T; 0 U; 0 Other;

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ö CAAGCGCGTGCGTGCATGATAGCGAAGAAAAAGCTATCCGTTTCAGTTAACTACTTAC 120 CAAGCGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCCGTTTCAGTTAACTACTTAC 120 180 GIGIGITIGICITITITITITITITITICGCIGIGCCTTTAICGCAAACAAGAAC 240 480 9 9 TGATAAAACTAGAAAATATCTTGAGAAACTTGTTTTCGCGCGTTTTTCGTTAATTGCC 300 TGATAAAACTAGAAAATATCTTGAGAAACTTGTTTTCGCGCTTTTCTTTTTGCTAATTGCC 300 GATCGCGGAAGAGAAAAAACAAGCAGTAGACAAAACAAGTGTGGTAATACAATCTGAAAAG 360 420 420 480 540 540 GGCACGAGGCGAACGATTTAAAGTGAGAAAAGAAACGGGTAAATCAGAGATCCCAAG CAAGATTGAATTTCGCCATCGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACT GGCACCATCAGCAGCCCGAGGGGTTTATCTATAGATGTCGCAGCTTATCATCTCATGC TGTCTGTGAGGTTGTTCTGTGTGCTCGTGTAGTATCTTAAATACATAGAGTGTGTTCATA Gaps . 0 DB 6; Length 2148; Indels ; 0 Query Match
100.0%; Score 2148;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2148; Conservative 0; Mismatches 61 61 121 121 181 181 241 241 301 301 361 361 421 421 481 481

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à	781 GTCGTTGCCATTCTCGCACTAACGATCTGGCAGACAACGCGTGTATCGC	CTGGACAAG 840
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δ	841 GAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCGGTTGG	ATAAACTAT 900
qq	841 GAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTTGG	
oy Db	901 CTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCGACTATCCAAAA 960 	TATCCAAAA 960 TATCCAAAA 960
ò	961 AAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGGTC	GATTCCATT 1020
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ð i	1081 GAGGACTACACCGATATGTTAAATAAACTCAACAATGCACATACCGGCACCACGCCCACA 114	ACGCCCACA 1140
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අ	1141 TCTGAGACCACTGCTGAGGGCGAGGCGAGACGGACAGTGCATCCTCAG	TCAAATGAT 1200
λ̈	1201 GACAATGTGTTCGATGACTTTACCAGCTACAATGCCCACAAAAAGAAGG	GAGAGAAA 1260
අු	1201 GACAATGTGTTCGATGACTTTACCAGCTACAATGCCCACAAAAAGAAGCA	GAGAGAAA 1260
ò	1261 TCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATTCAAGGAAA	CACACAGAG 1320
Ωp	1261 TCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATTCAAGGAAA	CACACAGAG 1320
8 o	1321 CTTCAGGAAAAGTCATCCAATGAGGCAACTTCCCAAAGAGGCCTGCACCACTTCACCAC 136	CTTCACCAC 1380
ò	81	CCGAGGAC 1440
ΩÞ	81	
δλ	1441 TCGAGGCCAGCAGTTTCCACTTGAGCAGCAGCGGGGGGTCACCAAGG	AGTATGGGC 1500
Db	1441 TCGAGGCCAGCACTTTCCACTTGAGCAGCAGCGGCGTCACCAAGG	 AGTATGGGC 1500
δ	1501 TACCATGGAGATATGTACATAGGAAAATGATAACGAGAGAAAACTCTTATCA	3GACACTTT 1560
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ò a	1561 CAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTATATACGT 1661 CAAACGCGCGTGACGGTGACCAATACAGGCTTAACGT 1661 CAAACGCGCGTGACGGTGACGGTGACGAGGTGACGAGGTGACGTGAGGTGACGGTGAGGTGACGGTGAGGTGACGGTGAGGTGACGGTGAGGGTGAGGGTGAGGGTGAGGGGGG	TACGCCCAG 1620
3 3		raceccae 1620
3	1621 ATATGCTACAACAACTCGCACGACCAGAACGGATTTATCGTCTTTCAAGGAGACACTCCA	BACACTCCA 1680

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2041 AGGAAAATCATATTTATTTTGTATATACTCGTTCGACTCTAAAAAGTGAATAAAATATA 2100
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                                                                                                                GATCGCAATGCCAGTTCTGCGGGGGGGAAACAACGGAAGCTACTTTGGCATCTTCAAGGTG
                                                                ACGAGTGGTCTGATCCACCTGGAACGAAACGAGGATCCATCTGAAGGACATTCACAAC
                                                                          ACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCATCTGAAGGACATTCACAAC
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/note= "Specifically claimed in claim 14"
652. .1881
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652. .807
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808. .1878
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The invention describes an isolated tumour necrosis factor polypeptide and polynucleotide are useful in controlling agriculturally important pests, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polynucleotide are useful for modulating controlling modified and polynucleotide are useful for modulating the polypeptide and polynucleotide may be useful for treating.

Thus controlling or preventing X-linked anhidrotic (hypohidrotic) ectodermal or spalaria and X-linked anhidrotic (hypohidrotic) ectodermal dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal or sweat like disorders, e.g. sparse hair, abnormal or missing teeth or sweat cland aberrations in animals (e.g. insects and potentially humans), condotoxicis shock, inflammation, haemorrhagic necrosis of tumours, cytotoxicity and obesity-linked insulin resistance, all of which involve TNF molecules. This sequence encodes the drosophila melanogaster tumour necrosis factor (TNF) protein, described in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm
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20-MAR-2001; 2001US-00813329.
                                                            21-MAR-2000; 2000US-0190816P.
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CHEN J.
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GUAN B.
BOWEN M A.
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/product= "TNFv1"
/note= "Tumour necrosis factor var
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/note= "Specifically claimed in cl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes an isolated tumour necrosis factor polypeptide (TNF). The polypeptide and polynucleotide are useful in controlling agriculturally important peets, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polynucleotide are useful for modulating ceptubalial morphogenesis, cell-matrix adhesion in files and mammals. Thus the polypeptide and polynucleotide are useful for modulating the polypeptide and polynucleotide may be useful for treating, ameliorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorders, e.g. sparse hair, abnormal or missing teeth or sweat gland aberrations in animals (e.g. insects and potentially humans), endotoxic shock, inflammation, haemorrhagic necrosis of tumours, cytotoxicity and obesity-linked insulin resistance, all of which involve TNF molecules. This sequence encodes the drosophila melanogaster tumour necrosis factor variant 1(TNFV1) protein, described in the invention
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                               Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
           Drosophila melanogaster genomic polynucleotide SEQ ID NO 15892
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                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                 The sequence is that of an example randomising oligonucleotide which is used in the prepr. of mRNA encoding candidate polypeptides for the method of systematic polypeptide evolution by reverse translation (SpERT). The method provides a rapid way of isolating and identifying polypeptide ligands which bind to target mols. The polypeptide ligands can be used in inhibitors of target mol. The polypeptide ligands can be used in inhibitors of target mol. function, as probes, as sequestering agents, darug delivery whicles, modififers of hormone action and as catalysts.
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                                                                                                                                                                                                                                                                                                                                      translation
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by linking each polypeptide in sample mixt. to individualised mRNA
allowing further synthesis of selected polypeptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Systematic peptide evolution by reverse translation, SPERT; ligand, specific; inhibitors; probes; assay; cell sorting; ss.
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0
                                                                                                                                                                                                                                                                         Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer for 5' fixed sequence contg. T7 promoter and RBS
                                                                                                                                                                                                                                                                    Score 66.8; DB 2; Length 3
Pred. No. 3.5e-05;
0; Mismatches 187; Indels
                                                                                                                                                                                                                                                Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 U; 0 Other;
                                                                                                              Example; Page 55; 102pp; English
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(first entry)
(COLS ) UNIV OF COLORADO
                                                                                                                                                                                                                                                                                            Matches 179; Conservative
                                                                                                                                                                                                                          See also AAQ21830-Q21832
                                            WPI; 1992-080018/10
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                       Tuerk C;
                                                                  New method of
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                       Gold L,
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Synthetic

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SPERT is used to select novel polypeptides that bind the antibody of the epitope commonly recognised by the antisera from autoimmune mice which are the fip progeny of a cross of NZB and NZW parents (Portanova et al., J. Immunol. 144, 4633, 1990). The known epitope consists of ca. 10 amino acids at the N-terminus of the histone HZB protein. To make mRNA encoding candidate polypeptides a 5' fixed sequence composed of a 7' promoter sequence and a ribosome binding site which is recognised by both provaryotic and eukaryotic ribosomes, terminating in a restriction prokaryotic and eukaryotic ribosomes, terminating in a restriction prokaryotic sequence of example shown). A 3' fixed sequence of ca. 100 nucleotides lacking stop codons. In addition, a 3' sequence of ca. 100 nucleotides lacking stop codons. In addition, a 3' primer annealing site is provided so that CDNA synthesis can be accomplished on the mRNA recovered from partitioned ribosome complexes. See also AAQ36845-63. (Updated on 25-MAR-2003 to correct PN field.)
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48.9%; Pred. No. 3.5e-05;
Live 0; Mismatches 187; Indels
                                                                                                                                                                       Systematic polypeptide evolution by reverse translation - u of polypeptide ligand specific for desired target molecule.
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                                                           Smith
                                                                                                                                                                                                                                                                 Example 1; Page 84; 98pp; English.
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                                                       Tuerk C, Pribnow
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(UYRE-) UNIV RES CORP
                                                                                                                  WPI; 1993-076529/09.
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Matches 179; Conserv
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                                                    Gold L,
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AAF76910
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CACCACGCCCACATCTGAGACCACTGCTGAGGGCGAGGGCGAGGGAGACGGACAGTGCATCCTC 1187

1188 AGCCTCAAATGATGACAATGTGTTCGATGACTTTACCAGCTACAATGCCCACAAAAGAA 1247

1248 GCAGGA 1253

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolating a polypeptide ligand to a target molecule, useful for diagnostic assays, comprises partitioning candidate mixtures comprised of ribosome complexes or mRNA.polypeptide copolymers relative to their affinity to the target molecule.
                                                                                                                                                                          ligand isolation; systemic polypeptide evolution by reverse translation;
                                                                                                                   Sequence containing a 120 repeat of ACG flanked by fixed fragments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith JD;
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                                                         (first entry)
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Matches 179; Conservative
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TUERK C.
PRIBNOW D.
SMITH J D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuerk C,
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                                                         29-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2001
                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                        SPERT; 88.
AAF76910;
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The sequences given in AA172769-81 are oligonuclectides which were used to make mRNA encoding a candidate polypeptide, a 5' fixed sequence composed of a 17 promoter sequence and a ribosome binding site which is recognised by both prokaryotic and eukaryotic ribosomes, terminating in a restriction endonuclease site. The resulting nucleic acid was used in the method of the invention for preparing ligands of target molecules in which mixtures of ribosome complexes or mRNA.circle-solid.polypeptide copolymers (mRcs.pCs) are partitioned by affinity to the target and amplified to create candidate mixtures enriched in ribosome complexes or mRs.pCs with an affinity to the target. Are new those are termed SPERT (Systematic Polypeptide Evolution by Reverse Translation). The SPERT methods are useful for isolating polypeptide ligands for desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New methods (termed SPERT (Systematic Polypeptide Evolution by Reverse Translation)) for selecting high-affinity polypeptide ligands that specifically bind target molecules, e.g. proteins, carbohydrates, toxins,
                                                                                                                                                                                                                      17 promoter; ribosome binding site; RBS; prokaryotic; eukaryotic; ribosome; mRNA.circle-solid.polypeptide copolymer; mRcs.pC; SPERT; Systematic Polypeptide Evolution by Reverse Translation; assay; diagnosis; cell sorting; inhibitor; probe; sequestering agent;
                                                                                                                                                                                         Oligo #7 for cloning T7 promoter and RBS containing mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 21; 38pp; English.
                                                                                    AAI72775 standard; DNA; 390 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-00561968.
91US-00739055.
98US-00197649.
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                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                ribosome complex; ss.
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CGACGA 367
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TUERK C.
PRIBNOW D.
SMITH J D.
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23-NOV-1998;
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CGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGG 1007

948 62

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888 GGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCAT 947

1008 TCTGGATTCCATTGCGGACGACGAGGACGACGATTAGCTATAGCTCTGTGGATGATGT 1067

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target molecules. The polypeptide products are useful for any purpose to which a binding reaction may be put, for example in assay methods.

C diagnostic procedures, cell sorting, as inhibitors of target molecule function, as probes, as sequestering agents and the like. In addition, polypeptide products of the invention can have catalytic activity. Target molecules include natural and synthetic polymers, including proteins, complexities, and small molecules, but and cell surfaces, coplysaccharides, glycoproteins, hormones, receptors and cell surfaces, cot transition state analogues and toxins. The novel SPERT method involves utilizing a candidate mixture of polypeptides having a randomized amino acid sequence. Each member of the mixture is linked to an individualized mRNA, which encodes the amino acid sequence of that polypeptide. The candidate polypeptides are partitioned according to their property of candidate polypeptides are partitioned according to their property of binding to a given desired target molecule. The partitioning is carried out in such a way that each mRNA encoding a polypeptide is partitioned exactly together with the means for further amplifying it by an in vitro process. Ultimately, both the desired optimal polypeptide are started and the mRNA encoding the polypeptide are considered, allowing further synthesis of the selected oplypeptide as desired, and further synthesis of the selected oplypeptide as desired, and further amplification of the coding sequence of the reference property of the means for in chemistry) in order to produce it in the analyse the amino acid sequence of the acide.
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Length 390; Score 66.8; DB 6; Length 3 Pred. No. 3.5e-05; 0; Mismatches 187; Indels Sequence 390 BP; 125 A; 126 C; 133 G; 6 T; 0 U; 0 Other; 3.1%; Query Match 3.1 Best Local Similarity 48.9 Matches 179; Conservative

involved in plant resistance or response to pathogenic infection. Mi comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to

invention

illustrate the

present invention relates to a method (M1) for identifying genes

Claim 27; SEQ ID NO 5263; 899pp; English

gene expression

Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or vixal infection by determining or detecting plant

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Hou Y;

SA, Zhu

Glazebrook J, Goff Whitham S, Xie Z,

κ'n

Cooper ;

Chen W, Co

Chang H, Katagiri

WPI; 2003-175290/17

(SYGN) SYNGENTA PARTICIPATIONS AG.

22-JUN-2001; 2001WO-IB001105 22-JUN-2001; 2001WO-IB001105

WO2003000898-A1

03-JAN-2003

Oryza sativa

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               888 GGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCAT 947
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Plant, bacterial infection; fungal infection; viral infection; rice; gene; ds.

ADA71938 standard; DNA; 2000 BP.

(first entry)

20-NOV-2003

ADA71938;

Rice gene, SEQ ID 5263

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(BALL/) BALLESTAS M E. (KAYE/) KAYE K M.
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                                        1250 AGGAGAGAAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATTCAAGGAA 1309
                                                                              1310 ATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACTTCCAAAGAGAGCCCTGCAC 1369
                                                                                                                    1370 CACTTCACCACCGTCGCAGAATGCATTCCCGCCATCGCCACCTCCTAGTCCGCAAAGCCA 1429
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                                                                                                                                                                                                                                                  Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus; latency-associated nuclear antigen; LANA; gamma-2 herpes virus; HHV8; rhadino virus cis-acting element; RVCAE; Kaposi's sarcoma; primary effusion lymphoma; PEL; human immunodeficiency virus; HIV; multicentric Castleman's disease; ds.
                                                                                                                                                                       728 RYWTSWYKYCKCSWKYRSMWYYWSWWWAKTWMMWRRYATRMMWWYRYSMKWYTWCTMWG
               493 RSGMKRKCRRRRWGRMYRMKRYYMSARYTMRYCARKK----YSYSAARKARCWYRGKG
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(KSHV) latency-associated nuclear antigen (LANA) gene. KSHV is also known as Human Herpes virus 8 (HHV8) and belongs to the rhadino virus, or gamma 2 herses virus class. The LANA protein is necessary for the efficient persistence of rhadino virus DNA in mammalian cells. Persistent rhadino virus infection is implicated in a variety of diseases e.g. Kaposi's Sarcona (KS). Primary Effusion Lymphoma (PBL) and multicentric catlement's disease. In addition, KS is a common malignancy in HIV patients. KSHV persists in host cells in a latent form. One of the few genes expressed from the latent viral DNA is LANA associates with both human chromosomes and with the rhadino virus cis-acting element (RVCAB), thereby providing a tethering function: the KSHV DNA episome is "tied" to the host cell. The present sequence may be used to screen and identify molecules that inhibit LANA interaction with RVCAB, thereby interfering with the latency cycle of this virus. Potential antiviral treatments for the above mentioned diseases may therefore be based on LANA deregulation.
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                                                                                                                                                                                          Treating or preventing a disease associated with rhodino virus infection in a mammal which includes Kaposi's Sarcoma and Primary Effusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1107 CGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is the Kaposi's sarcoma-associated herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55.8; DB 3; Length 3
Pred. No. 0.027;
0; Mismatches 132; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Updated on 15-SEP-2003 to standardise OS field)
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Kaye KM
                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 6; 70pp; English
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(revised)
(first entry)
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Matches 135; Conservative
Ballestas ME,
                                                                       WPI; 2000-387829/33.
P-PSDB; AAY96255.
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29-JUN-2001
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us-09-813-329-5.rng

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The invention provides a composition comprising nucleic acid, histone HI forcein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone HI protein, where the tethering protein is LANA. The composition is useful in aiding the retention of the viral DNA in the host cell. The viral vector encodes a protein suitable for tethering DNA to Histone HI. Methods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histone HI and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis. Parkinson's disease, Huntington disease and diabetes. The present sequence represents the nucleotide sequence of the Kaposi's sarcoma associated herpesvirus (human herpesvirus 8) latency-associated nuclear accidents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                A composition for use in gene therapy comprises an expression vector that includes a nucleic acid sequence encoding a nucleic acid binding protein.
Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigen (LANA), which acts as a tethering protein. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-SEP-2003 to standardise OS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3489 BP; 1053 A; 862 C; 1137 G; 437 T; 0 U; 0 Other;
                   KSHV; latency-associated nuclear antigen; LANA; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              composition for use in gene therapy
                                                                                               Location/Qualifiers
1. .3489
/*tag= a
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                                                                                                                                                                                                                                                    29-SEP-2000; 2000WO-US026908
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nes 135; Conservative
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                                                           herpesvirus 8.
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                                                             Human
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987 GGATGATGAGGAGGAGCAGGAGACAGATGAGGAGGACGAGGATGACGAGGATGA 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a system (A) for maintaining a plasmid as an episome in mammalian cells, comprising the rhadinoviral sequence LANA (latency-associated nuclear antigen) of 3489 base pairs (see ABA33487, S1) expressed in the cell, and the rhadinoviral sequence RVCAE (rhadinoviral cis-acting element) of 801 base pairs (see ABA3348, S2) present in the plasmid. Also describes is a method for maintaining a closed circular DNA in a cell by expressing (S1) in the cells and having particularly used in gene therapy (or other gene transfer applications) particularly used in gene therapy (or other gene transfer applications) persistence of gene therapy vectors in cells. The present sequence encodes Kaposi's sarcoma-associated herpesvirus (KSHV, also called human herpesvirus 8) LANA protein, which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  System for episomal retention of plasmids in mammalian cells, useful in gene therapy, comprises rhadinoviral LANA and RVCAE sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           828 GCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTT
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                                                                                                                   Kaposi's sarcoma-associated herpesvirus LANA protein encoding DNA
                                                                                                                                                    Kaposi's sarcoma-associated herpesvirus; KSHV; LANA; RVCAE; PEL; KSHV terminal repeat; rhadino virus cis acting element; episome; primary effusion lymphoma; latency-associated nuclear antigen; gene therapy; gene transfer; gene; ds.
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                                                                                                                                                                                                                                                                                              1. 3489
/*toad
/product= "LANA protein"
/note= "latency-associated nuclear antigen"
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Pred. No. 0.027;
0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                            Location/Qualifiers
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                BP.
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            ABA93487 standard; DNA; 3489
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                                                                                                                                                                                                                                           Human herpesvirus 8.
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P-PSDB; ABB05621.
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                                                                                  25-APR-2002
                                               ABA93487;
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27-AUG-2003
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This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for ORF65 which encodes capsid protein IV, ORF67, Which encodes tegument protein IV, ORF68 which encodes a glycoprotein, ORF93 which encodes kaposin, KI3, ORF72 which encodes glycoprotein, ORF93 which encodes immediate early protein (IEP), KI4 which encodes (V-adh), ORF74 which encodes G-protein coupled receptor, ORF75 which encodes tegument protein/FGARAT, KI5. KSHV is a new human Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the most common form of neocuring in persons with acquired immune deficiency diagnosis and treatment of a subject with Kaposi's sarcoma and for detecting expression of a DNA virus associated with Kaposi's sarcoma in a
                                                                                                                                                                                                                                                                                                                              Kaposi's sarcoma, acquired immune deficiency syndrome, AIDS, DHFR, Bcl-2; dihydrofolate reductase, LUR; long unique region; vaccine; prophylaxis; diagnosis; treatment; HHVB; capsid protein IV; tegument protein IV; glycoprotein; kaposin; cyclin D; immediate early protein; IEP; OX-2; v-adh; G-protein coupled receptor; FGARAT; ds.
                                            TCTGGATTCCATTGCGGACGACGACGACGACGACGTTAGCTATAGCTCTGTGGATGTGT
                                                                       or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaposi's sarcoma-associated herpes virus nucleic acid - encodes
di:hydro:folate reductase and is useful for treatment, prophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32207 BP; 7229 A; 9156 C; 8713 G; 7109 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Edelman IS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detecting expression of a DNA virus associated with Kacell. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chang Y,
                                                                                                                                                                                                                                                                                                     KSHV LUR DNA (nucleotides 105,301-137,507).
                                                                                                   TGGCGCAGACTACGAGGACTACACCGA 1094
                                                                                                                              GGACAATGAGGACGAGGATGACGA 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Col 155-182; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Russo JJ,
                                                                                                                                                                                         805/c
AAV73805 standard; DNA; 32207 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis of Kaposi's sarcoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-00770379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-00770379
                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                            (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Human herpesvirus 8.
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                                                                                                                                                                                                                                                                       GGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCAT
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90173. .90643
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89600. .90541
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/product= "glycoprotein M"
complement(69412. .69915)
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complement(17261. .17875)
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complement(88410, .88910)
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/product= "interleukin 6"
complement(21548. .21832)
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Best Local Similarity 50.6 Matches 135; Conservative

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New nucleic acid encoding Kaposi's sarcoma associated herpes virus proteins – useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV patients.
                        /product= "interferon regulatory factor 4" complement(111931. .112443)
                                                                                                                                                                                                                              Moore PS;
                                                              /*tag= n
/product= "immediate early protein"
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                                                "capsid protein IV"
                                                      complement (123808. 127296)
 /product= "glycoprotein X"
complement(93636. .94127)
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96US-00687253.
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13-NOV-1996;
13-NOV-1996;
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This sequence represents the long unique region and terminal repeat of the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known as human herpes virus 8 (HHVB). This sequence contains the DNAs of the invention which encode KSHV polypeptides selected from: (a) viral interleukin-6 (IL-6); (c) viral IRF1; (d) complement-binding protein; glycoproteins B, M or L; (d) capsid protein IV encoded by ORF5; and (e) immediate early protein ecoded by ORF73. Labelled probes for the nucleic acid, proteins encoded by IL and antibodies (Ab) specific for the proteins are useful for chetecting HHVB, specifically for diagnosis of Kaposi's sarcoma, in body cluids or tissue samples. HHVB infections can be treated with antisense or triplex forming molecules or agents that bind specifically to the protein. Ab may be used for prophylaxis or treatment of HHVB infection, while the protein can be used in protective vaccines. Ab may also be used to differentiate between lymphomas, and HHVB may be inplicated in many coher lymphoproliferative diseases such as lymphomas, leukaemia, splenomegaly and mycosis fungoides. Cells and animals containing the nucleic acid are useful for fung screening. HHVB derived peptides can be inhibited with methotrexate. These can also be used to determine the immune status of a patient infected with HIV. HYPB derived protein cural MIP III may be used as an anti-inflammatory agent for, e.g. treating rheumatoid arthritis. This sequence is stated as containing 81 correcting copen reading frames. (Updated on 27-AUG-2003 to correct OS field.)

828 GCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTT 887 0; Gaps Score 55.8; DB 2; Length 137507; Pred. No. 0.12; 0; Mismatches 132; Indels 0; Query Match 2.6%; Best Local Similarity 50.6%; Matches 135; Conservative

Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 U; 0 Other;

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126250 CAAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGATGACGAGGATGA 126191
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888 GGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCAT 947
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-410-399-1

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US-08-770-669A-20

US-08-98-96-7

US-09-18-847-112

US-09-98-847-112

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US-09-54-37-1

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Sequence 7, Application US/09197649

Patent No. 6194550

GENERAL INFORMATION:

APPLICANT: Gold, Larry

APPLICANT: Fribnow, David

APPLICANT: Pribnow, David

APPLICANT: Pribnow, David

APPLICANT: NAVO2/C1-CON

CURRENT APPLICATION NUMBER: US/09/197,649

CURRENT PELING DATE: 1992-01-31

EARLIER APPLICATION NUMBER: 07/739,055

EARLIER PILING DATE: 1991-08-01

EARLIER APPLICATION NUMBER: 07/561,968

EARLIER APPLICATION NUMBER: 07/561,968

EARLIER APPLICATION NUMBER: 07/561,968

EARLIER PLING DATE: 1990-08-02

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
              Sequence 24, Appl
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Sequence 26, Appl
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Sequence 16317, A
Sequence 16317, A
Sequence 16324, A
Sequence 11, Appl
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                                                                          1167 CGAĞGAGGACGAÇĞAĞĞAĞĞAÇĞAĞĞAĞĞAĞĞAĞĞAĞĞAĞĞAĞĞAĞĞATĞATĞATĞA
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Patent No. 6482587
GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA TITLE OF INVENTION: to Genomic Host DNA FILE REFERENCE: UM-03778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                887
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APPLICANT: Kaleff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
TITLE OF INVENTION: HAADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT APPLICATION WUMBER: US/09/298,568
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
                                          CGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGG
                                                                                                                                1008 TCTGGATTCCATTGCGGACGACGAGGACGACGACGTTAGCTATAGCTCTGTGGATGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                                       1068 TGGCGCAGACTACGAGGACTACACCGA 1094
                                                                                                                                                                                                                                                                 1227 GGACAATGAGGACGAGGAGGATGACGA 1253
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Matches 135; Conservative
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                                                   888 GGGCATAAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCAT 947
                                                                                               1188 AGCCTCAAATGATGACAATGTGTTCGATGACTTTACCAGCTACAATGCCCACAAAAAAA
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                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08728323A

Patent No. 5946676

GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Belenan, Isidore S.
APPLICANT: Belenan, Isidore S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's TITLE OF INVENTION: Brooding Same And Uses Thereof
NUMBER OF SEQUENCES: 2
ADDRESSEE: Cooper & Dunham ILP
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llarity 50.6%; Pred. No. 0.00063;
Conservative 0; Mismatches 132; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:

CLASSIFICATION: 435

ATTONNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS

TELECOMMULICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEPHONE: 212-391-0525

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3489 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: DNA (genomic)
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STATE: New York
COUNTRY: U.S.A.
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US-08-728-323A-1
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Best Local Simi
Matches 135;
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Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Rohensy, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Belman, Isladors S.
APPLICANT: Moore, Patricks.
APPLICANT: Moore, Patricks.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                     Length 3489;
                                                                                                                                                                                                                   2.6%; Score 55.8; DB 4; Length 3 50.6%; Pred. No. 0.00063; tive 0; Mismatches 132; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
                                                                                                                             TYPE: DNA; Caposi's sarcoma-associated herpesvirus US-09-410-399-1
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CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 1
LENGTH: 3489
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1185 Avenue of the Americas
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/DOCKET NUMBER: 5234:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: FLOPDy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
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Matches 135, Conservative
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CLASSIFICATION: 435
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STATE: New York
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                       828 GCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGTTT
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                                                                                                                                                                                     Query Match 2.6%; Score 55.8; DB 2; Length 32207; Best Local Similarity 50.6%; Pred. No. 0.0019; Matches 135; Conservative 0; Mismatches 132; Indels 0;
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APPLICANT: Bohenzky, Roy A.
APPLICANT: Busso, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20770 GGACAATGAGGACGAGGAGGATGACGA 20744
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STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-F
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/757,669P
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-757-669A-20/c
; Sequence 20, Application US/08757669A
Patent No. 6183751
; GENERAL INFORMATION:
                                                                                                           MOLECULE TYPE: DNA (genomic)
LENGTH: 32207 base pairs
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                               TYPE: nucleic acid STRANDEDNESS: double
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                        linear
                                  ; TYPE: nucl;
; STRANDEDNES;
; TOPOLOGY:
; MOLECULE TYPE
US-08-770-379-20
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1068 TGGCGCAGACTACGAGGACTACACCGA 1094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (936)
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NAME/KEY: SITE
LOCATION: (946)
FEATURE INFORMATION: n
FEATURE:
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                 20950 CGAGGAGGATGACGAGGATGACGAGGATGACGAGGAGGATGATGACGAGGAGGATGA
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APPLICANT: Chang, Yuan
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Russo, James J
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
FILE REPERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT PLING DATE: 1999-11-17
PRIOR FILING DATE: 1997-07-22
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                                                                                                                                                                    828 GCATCTGGACAAGGAGCTGAAGACCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTT
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                                                                                        Query Match 2.6%; Score 55.8; DB 3; Length 32207; Best Local Similarity 50.6%; Pred. No. 0.0019; Matches 135; Conservative 0; Mismatches 132; Indels 0;
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ORGANISM: Kaposi's sarcoma-associated herpesvirus
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Sequence 20, Application US/09230371A
Patent No. 6348586
. 10FOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-669A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.6%;
Matches 135; Conservative
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US-09-230-371A-20
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SEQ ID NO 20
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2026 TTAGTCAGAAGACGGAGGAAAATCATATTTATTTTGTATATACTCGTTCGACTCTAAAAA 2085
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Patent No. 5936078
GENERAL INFORMATION:
APPLICANT: Kuga Ttesro
APPLICANT: Nakagawa Satoshi
APPLICANT: Sakaki yoshiyuki
APPLICANT: Zhao Nanding
APPLICANT: Hashida Hideji
TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE
TITLE OF INVENTION: AND NOVEL ANTIBODY
                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                                                                     FILE KEKEKENCE: FZOALFLE
CURRENT PAPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1998-07-30
EARLIER PELING DATE: 1998-07-30
EARLIER PILING DATE: 1998-08-05
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20770 GGACAATGAGGACGAGGAGGATGACGA 20744
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-112
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Patent No. 6476195
GENERAL INFORMATION:
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Best Local Similarity 64.1:
Matches 75; Conservative
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ORGANISM: Zea mays
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SEQ ID NO 10211
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                                    LENGTH: 299
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
ITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                       CITY: New York
COMPUTE: New York
COMPUTE: New York
COMPUTE: New York
COMPUTE: State State State State State: New York
COMPUTE: State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State State
                                                                     CELLA, HARPER AND SCINTO
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TELEX: 236262
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3527 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
TELEPHONE: 212-758-2400
TELEFAX: 212-758-2982
                             CORRESPONDENCE ADDRESS:
ADDRESSEE: FITZPATRICK,
STREET: 277 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 140 to 1084
LDENTIFICATION METHOD:
US-08-909-965C-7
NUMBER OF SEQUENCES: 17
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IMMEDIATE SOURCE:
CLONE: F998
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US-09-621-976-10211
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                                                                                        Score 50.6; DB 4; Length 299; Pred. No. 0.0036; 0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Mahajan, Pramod B.
APPLICANT: Tagliani, Laura
TILE OF INVENTION: Maize Rad23 Genes and Uses Thereof
FILE REFERENCE: 0964
CURRENT APPLICATION NUMBER: US/09/413,574
CURRENT APPLICATION NUMBER: 60/109,728
EARLIER APPLICATION NUMBER: 60/109,728
EARLIER FILING DATE: 1999-11-23
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/09372422A
Sequence 39, Application US/09372422A
Sequence 39, Application US/09372422A
Sequence 39, Application
TUPOR TUPORMATION:
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
TITLE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT APPLICATION NUMBER: US 60/098,692
PRIOR APPLING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-413-574-1
; Sequence 1, Application US/09413574
; Patent No. 6235972
                                                                                          Query Match
Best Local Similarity 65.5%;
Matches 74; Conservative
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Matches 92; Conservative
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; LOCATION: (58)...(1272)
US-09-413-574-1
TYPE: DNA
ORGANISM: Homo sapiens
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; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-182-816-24
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Best Local Similarity 68.0%
Matches 70, Conservative
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Best Local Similarity 68.09
Matches 70; Conservative
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; LOCATION: (159)..(1553)
US-09-471-528-22
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                                                                                                                                                                                                                                                                              RESULT 13
US-09-182-816-22
i Sequence 22, Application US/09182816
j Patent No. 6143542
j GENERAL INFORMATION:
i APPLICANT: Wisnewski, Nancy
i APPLICANT: Silver, Gary M.
i APPLICANT: Lo, Katherine C.
i TILLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES,
i TILLE OF INVENTION: PROTFINS AND USES THEREOF
i TILLE OF INVENTION: PROTFINS AND USES THEREOF
i CURRENT APPLICATION NUMBER: US/09/182,816
i CURRENT APPLICATION NUMBER: 08/989,510
i EARLIER PILLER FILLING DATE: 1999-10-29
i EARLIER PILLING DATE: 1999-10-29
i EARLIER PILLING DATE: 1997-12-12
i SOFTWARE: PATENTIN Ver. 2.0
i SEQ ID NOS: 31
i SEQ ID NO 2.
i ENGREUT.
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SOFTWARE: FRSTSEQ for Windows Version 3.0
SEQ ID NO 39
LENGTH: 1485
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Patent No. 613542
GENERAL INFORMATION:
APPLICANT: Wisnewski, Nancy
APPLICANT: Wisnewski, Nancy
APPLICANT: Lo. Katherine C.
APPLICANT: Brandt, Revin S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Ctenocephalides felis
                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (133) ... (1015)
US-09-372-422A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (159)..(1553)
US-09-182-816-22
                                                                         TYPE: DNA
ORGANISM: Zea mays
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US-09-182-816-24/c
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## Sequence 22, Application US/09471528

## Sequence 22, Application US/09471528

## Sequence 22, Application US/09471528

## Sequence 22, Application US/09471528

## SPELICANT: Wisnewski, Nancy

## APPLICANT: Silver, Gary M.

## APPLICANT: Silver, Gary M.

## APPLICANT: Silver, Gary M.

## APPLICANT: Silver, Gary M.

## APPLICANT: Develope and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provided and the provi
TITLE OF INVENTION: NOVEL FLEA EPOXIDE HYDROLASE NUCLEIC ACID MOLECULES, FILE REFERENCE: FC.3-CL.
CURRENT APPLICATION NUMBER: US/09/182,816
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 08/989,510
EARLIER FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 1736
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Sequence 9339, Ap Sequence 6106, Ap Sequence 1285, Ap Sequence 26900, A Sequence 24712, A Sequence 31149, A Sequence 11695, Sequence 11695, Sequence 11693, Ap Sequence 2117, App Sequence 2117, App Sequence 3766, Ap Sequence 17202, A Sequence 1931, App Sequence 1931, App Sequence 118975, Sequence 15014, A Sequence 118975, Sequence 118975, Sequence 118976, A Sequence 11054, A Sequence 1105

17579, A 9339, Ap 60658, Ap 1285, Ap 26900, A 2472, A 93967, A 911695, 11695, 81149, A 8968, A

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-813-329-1
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US-10-424-599-9903
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	RESULT 1 US-09-813-329-5 Sequence 5, Application US/09813329 Sequence 5, Application US/09813329 Sequence 5, Application US/09813329 Sequence 5, Application US-00012968A1 SEMERAL INFORMATION: TITLE OF INVENTION: No. US-000012968A1e1 Drosophila Tumor Necrosis Factor Class TITLE OF INVENTION: Variants Thereof FILE REPERENCE: D0016.np CURRENT APPLICATION NUMBER: US/09/813,329 CURRENT FILING DATE: 2001-03-20 SRIOR APPLICATION NUMBER: 60/190,816 SRIOR APPLICATION NUMBER: 60/190,816
ve a printed,	NUMBER OF SEQ ID NOS: 65 SOFTWARE: PatentIn version 3.0 SEQ ID NO 5 LENGTH: 2148 TYPE: DNA
tion	/ NONTURE: / FEATURE: / NAME/KEY: CDS / LOCATION: (634)(1860) US-09-813-329-5
ce 5, Appli ce 1, Appli ce 3, Appli ce 7, Appli	Query Match 100.0%; Score 2148; DB 9; Length 2148; Best Local Similarity 100.0%; Pred. No. 0; Matches 2148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
nce 46034, A nce 1, Appli nce 1, Appli	Qy 1 GGCACGAGCGAACGGACGTTTAAAGTGAGAAAGAAACGGTAAATCAGAGATCCCAAG 60
nce 483, App nce 606, App nce 9903, Ap nce 82347, A	Qy 61 CAAGCGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCGGTTTCAGTTAACTTAC 120 Db 61 CAAGCGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCGGTTTCAGTTAACTACTAC 120
nce 38982, A nce 287, App	Qy 121 CAAGATTGGAATTTCGCCATCGGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACT 180

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ALIGNMENTS

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Qy	181 GTGTGTTTTTTTTTTTTTTTTGGTTTTGGTGGCTTTATGGCAAACAAGAAC 240 	VO da	1261 TCTCGCTCGATTGCCGATGTACGCAATGAGGAGAATATTCAAGGAATCACACAGAG 1320
Qy Dp	30	QV Op	1321 CTTCAGGAAAAGTCATCCAATGAGGCAACTTCCAAAQAGAGCCCTGCACCACTTCACCAC 1380
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& 8	1081 GAGGACTACACCGATATGTTAAATAAACTCAACAATGCACATACCGGCACCACGCCCACA 1140 1081 GAGGACTACACCGATATGTTAAATAAACTCAACAATGCACATACCGGCACCACGCCCACA 1140	RESULT US-09-E	2 813-329-1 ence 1, Application US/09813329
çy Db	1141 TCTGAGACCACTGCTGAGGGCGAGGGCGAGGGCACAGTGCATCCTCAGCCTCAAATGAT 1200	, Pate ; GENE ; APP	; ;
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                                                                         CTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCGACTATCCAAAA
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98.4%; Score 2112.8;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2126; Conservative 0; Mismatches
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; SEQ ID NO 1
; TYPE: DNA
                                                                                             ORGANISM: Drosophila melanogastor
                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (652)..(1878)
US-09-813-329-1
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Qy 1054 TCTGTGGATGATGTTGGCGCAGACTACGAGGACTACCGATATGTTAAATAAA	00 00 00 00 00 00 00 0	RESULT 4 US-09-790-399-7 US-09-790-399-7 Sequence 7, Application US/09790399 Patent No. US20020038000A1 GENERAL INFORMATION: APPLICANT: Gold, Larry APPLICANT: Bribnow, David APPLICANT: Bribnow, David TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation FILE REFERENCE: NEX02/C1-CON2 CURRENT APPLICATION WUMBER: US/09/790,399 CURRENT FILING DATE: 2001-02-22 PRIOR APPLICATION NUMBER: 09/197,649 PRIOR APPLICATION NUMBER: 09/197,649
QY 1921 CGACTGCTGGATGCGATTCATCGCCAGCGTGAATCCATTAGTTCGTAGTACCTAGTC 1980 Db 1939 CGACTGCTCGTGAATGCGATTCATCGCCAGCGTGATTCGTTAGTTCGTTGTC 1988 QY 1981 TTAGTCACTCCAAACCTAATTCATCGCATTGGCATTAGTCAGAAGACG 2040 Db 1999 TTAGTCACTCCAAACCTAATTCTCAATCGGATACTGCATTAGTCAGAAGACG 2058 QY 2041 AGGAAAATCATATTTTTTTTTTTTTTTTTTTTTTTTTTT	SEQUENCE 3 Sequence 3. Application US/09813329 Patent No. US20020012968A1 GENERAL INFORMATION: Patent No. US20020012968A1e1 GENERAL INFORMATION: APPLICATION: APPLICATION: APPLICATION: APPLICATION NUMBER: US0020012968A1e1 Drosophila Tumor Necrosis Fact FRICK FILING DATE: CURRENT FILING DATE: CURRENT FILING DATE: CURRENT FILING DATE: CURRENT FILING DATE: COOF-03-21 SEQ ID NOS: 65 SEQ ID NOS: 65 SEQ ID NOS: 65 SEQ ID NOS: 65 SEQ ID NOS: 66 SEQ ID NOS: 67 SEQ ID NOS: 68 SEQ ID NOS: 69 SEQ ID NOS: 69 SEQ ID NOS: 60 SEQ ID NOS: 60 SEQ ID NOS: 61 SEQ ID NOS: 63 SEQ ID NOS: 64 SEQ ID NOS: 65 SEQ ID NOS: 66 SEQ ID NOS: 67 SEQ ID NOS: 68 SEQ ID NOS: 69 SEQ ID NOS: 69 COCANIEN: NAME/KEY: COS NAME/KEY: COS CONTINENT APPLIATION OF SEQ ID NOS: 634 ATGACTGCCGAAGCGCCTTATAACGCCAACGACGCCAACGACGACTATTTTTTTT	Qy 814 ACAACGCGTGTATCGCATCTGGACAAGGAGCCTGAAGCGTGCTCGATAAT 873 Db 161

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615 CGACGACGATGAAGACGAAGAAGAAAGTGATGT 650
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Matches 147; Conservative
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ORGANISM: Glycine max
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Matches 147; Conserv
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     US-10-425-114-7734
                                   Query Match
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Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Goo, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

WUMBER OF SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                            Length 390;
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PRIOR FILING DATE: 1992-01-31
PRIOR APPLICATION NUMBER: 07/739,055
PRIOR FILING DATE: 1991-08-01
PRIOR FILING DATE: 1990-08-02
PRIOR FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 7
                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 46034, Application US/10424599
Publication Wo. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REPERENCE: 39-21(5323)8
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 1269
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      Length 966;
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53.3%; Pred. No. 0.00029;
tive 0; Mismatches 123;
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   Score 57.2; DB 13;
Pred. No. 0.00024;
0; Mismatches 123;
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2.7%;
ilarity 53.3%;
Conservative
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us-09-813-329-5.rnpb

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987 dGATGATGAGGAGGAGCAGGAGACGATGAGGAGGACGAGGATGACGAGGAGGATGA 1046
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                                                                    APPLICANT: Kieff, Eliott D.
APPLICANT: Kieff, Eliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Raye, Kemeeth M.
TITLE OF INVENTION: RIADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE TILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US 60/109/422
PRIOR PILING DATE: 2001-66-28
PRIOR FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN VOET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or Enhance the Binding of Viral DNA
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2.6%; Score 55.8; DB 13; Length 3489;
Best Local Similarity 50.6%; Pred. No. 0.0014;
Matches 135; Conservative 0; Mismatches 132; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Kaposi's sarcoma-associated herpesvirus
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ORGANISM: Kaposi's sarcoma-associated herpesvirus
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Publication No. US2003013394811
GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Mechods to Inhibit or Enl
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/10/294,804
PRIOR APPLICATION NUMBER: US/09/410,399
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PRECENTION NOS: 6
SOFTWARE: PRECENTION NOS: 6
SOFTWARE: PRECENTION NOS: 6
SOFTWARE: SEC ID NOS: 6
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Sequence 1, Application US/09894273
Publication No. US20040037847A1
GENERAL INFORMATION:
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DB 15; Length 3489;

Score 55.8;

2.6%;

Query Match

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JULY SEQUENCE 483, Application US/10311455

| Sequence 483, Application US/10311455
| Publication No. US20030143606A1
| Publication No. US20030143606A1
| Publication No. US20030143606A1
| APPLICANT: DEEK, Alexander
| APPLICANT: PIPEBNBROCK, Christian
| APPLICANT: BERLIN, Kurt
| TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determing ITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determing ITLE OF INVENTION: Cytosine methylation
| TITLE OF INVENTION: Cytosine methylation
| TITLE OF INVENTION: Cytosine methylation
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65.8%; Pred. No. 0.0047;
ive 0; Mismatches 41; Indels 0;
       Pred. No. 0.0014;
0; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1227 GGACAATGAGGACGAGGAGATGACGA 1253
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Best Local Similarity 50.6%;
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 79; Conserva
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US-10-225-567A-606
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TYPE: DNA ORGANISM: Glycine max
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LENGTH: 372
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APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: uS/10/225,567A

CURRENT PILING DATE: 2001-12-19

PRIOR PILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: Patentin version 3.1

SEQ ID NO 606

LENGTH: 1915
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Indels
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Local Similarity 77.4%; Pred. No. 0.0037;
Hes 65; Conservative 0; Mismatches 19;
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US-10-424-599-9903
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OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-606
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ORGANISM: Glycine max
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Page 7

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Zhou Yihua

TITLE OF INVENTION: David K

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 181016 and Uses Thereof for Plant Improvement

CURRENT APPLICATION WHOBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

LENGTH: 219

TYPP: LENGTH: 219
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Publication No. US2004003107241
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 372;
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US-10-424-599-38982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_45376C.1
US-10-424-599-82347
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1988 CTCCAAACCTAATCTCAATCGGAATCGTGCATACTGCATTAGTCAGAAGACGGAGGAAAA 2047
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GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Tillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US 60/191, 031
PRIOR APPLICATION NUMBER: US 60/191, 031
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-06-15
PRIOR PELING DATE: 2000-07-27
PRIOR PELING DATE: 2000-07-27
PRIOR PELING DATE: 2000-07-22
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PRIOR PELING DATE: 2000-07-22
PRIOR APPLICATION NUMBER: US 60/257, 672
PRIOR PELING DATE: 2000-07-22
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FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR APPLICATION NUMBER: DCT/US01/18569
PRIOR APPLICATION NUMBER: DCT/US01/18569
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
ENGIH: 1898
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Pred. No. 0.0023;
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NAME/KEY: misc feature

LOCATION: (1895)...(1895)

OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-287
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; Sequence 17579, Application US/09814353
; Publication No. US20030165831A1
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ORGANISM: Homo sapiens
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Best Local Similarity
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ORGANISM: Homo
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Search completed: September 15, 2004, 08:12:30 Job time : 4278 secs

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BI620499 RH91659.5
CK135985 SD18286.3
BIG35654 SD18286.3
BIG35692 SD17545.5
BK560278 BX560278
                                                                                                                                  BX560278 BX560278
BL108596 Drcsephil
BG553005 Adab62c09.
CD099026 AGENCOURT
BU711970 SJEELA02
BU711970 SJEELA02
BU711970 SJEELA02
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BU711192 SJEEJA08
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Ditera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 699)
1 (bases 1 to 699)
1 Lewis, S. and Rubin, G.M.
BOGP/HHMI Drosophila EST Project
Unpublished (2001)
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
estimated-cyto:46813-4684: 04/13/2001
Plate: SD.156 row: A column: 11
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AW134038
CB366950
CB366301
AZ528485
AZ67621045
BW249956
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CNS017WQ
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CK017088
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CD752688
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/clone_lib="SD Drosophila melanogaster Schneider L2 cell
culture_pOT2"
                            46E1-46E1;: 04/13/2001, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 A. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stour C. Stou
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/organism="Drosophila melanogaster"
/mol_type="mrNA"
/db xref="taxon:7227"
/clone="SD13795"
                                 on: 2R
                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
                            FBan0012919 located
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SD13795.5prime SD Drosophila melanogaster Schneider L2 cell culture
pOT2 Drosophila melanogaster cDNA clone SD13795 5 similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAGAAAATATCTTGAGAAACTTGTTTTCGCGCTTTTTCTTTTGCTAATTGCCGATCGCGGA 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAGATCCCCAGTGTTCATCAATTATGACTGCCGAGACCCTCAAGCCGTTTATATAACGCCA 659
                                                                                                                                                                                                                                                                                                                                                                               melanogaster Schneider L2 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pOT2; Site 1: EcoR1; Site 2: Xho1; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
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                                                                                          1. 699
/organism="brosophila melanogaster"
/mol_type="mkNA"
/db_xref="taxon:7227"
/clone="blost="blost="https://db.nost="blost="blost="https://db.nost="blost="blost="https://db.nost="blost="blost="https://db.nost="blost="blost="https://db.nost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="blost="bl
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BIG38827 10-SEP-2001 SD21218.5prime SD Drosophila melanogaster Schneider L2 cell culture port Drosophila melanogaster cDNA clone SD21218 5, mRNA sequence.
                                                                                                                                                                                                                                                                                                                      360 AGCAGCCCGAGGGGTTTATCTATATAGATGTCGCAGCTTATCATCTCATCTCTGTGA 419
                                                                                                                                                                                                                                                                                                                                                                                            300 AGAGAAAAACAAGCAGTAGACAAAACAAGTGTGGTAATACAATCTGAAAAGGGCACCATC 359
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I (bases I to 688)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.

BDGP/HHMI Drosophila EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540 ATCATCATCGTCGTCATTATCAACAGAATCAGCATCAGCATCTGGAGGCCCCGGTTGCTC
                   ATTTCGCCATCGGGCAAATTACTAAAAATACATAAGTGCAACTGCTCCACTGTGTTGT
                                                                                                                                                 TAGAAAATATCTTGAGAAACTTGTTTTCGCGCTTTTTCTTTTGCTAATTGCCGATCGCGGA
                                                                                                                                                                                    240 ragaaaararcirgagaaacrigirircececrirircririrecraarrecearcecea
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                                                                         GTTTTTTTTTTTTTTTGGTTTTTCGCTGTGCCTTTATCGCAAACAAGAACTGATAAAAC
                                                                                             G-TTTTTTTTTTTTTTGCTTTTCGCTGTGCCTTTATCGCAAACAACAACTGATAAAAAC
                                                                                                                                                                                                                         AGAGAAAAACAAGCAGTAGACAAAACAAGTGTGGTAATACAATCTGAAAAGGGCACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
hit gened AE003831: arm:2R [4876906,5137815]
Plate: SD.212 row: B column: 6
High quality sequence stop: 602.
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly)
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                                                                                                            TCATCGCCAGCGTGAATCCATTAGTTCGTAGTACCTAGTCTTAGTCACTCCAAACCTAAT 2000
                                                                                                                                                                                    GCAGGGAAACAACCGAAGCTACTTTGGCATCTTCAAGGTGTAAATTGGAGAGATTATCCC 480
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Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Brukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophila.
Drosophilaes; Drosophila.
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
Brospy, Hand Drosophila EST Project
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/clone_lib="SD Drosophila melanogaster Schneider L2 cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 466 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
estimated-cyto:46B13-46E4: 05/19/2001
Plate: SD.197 row: H column: 10
High quality sequence stop: 584.
Location/Qualifiers
1. 686
1. 666
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/db_xref="taxon:7227"
/clone="SD19794"
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B1637732.1 GI:15539942
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Mosptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 649)

1 (bases 1 to 649)

1 (barvey, D., Broketein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., BDGP/HHMI Drosophila EST Project

Unpublished (2001)
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                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"

/mol_type="mRNA"

/db xref="twon;7227"

/clone="SD12092"

/lab_host="DH5-alpha"

/clone_lib="SD Drosophila melanogaster Schneider L2 cell
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 466 6798
Fax: 510 466 6798
Fax: 510 466 6798
Fax: 510 466 6798
Fax: 510 686 6798
Father: SD-120 row: H column: 8
High quality sequence stop: 597.
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                                                                                                                             Contact: Stapleton, M.
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/db xref="taxon:/__.
/clone="SD21218"
/lab_host="DH5-alpha"
/clone_lib="SD Drosophila melanogaster Schneider L2 cell
culture pOT2"
/note="Vector: pOT2; Site 1: EcoR1; Site 2: Xho1; Sized
fractionated cDNAs were directly ligated_into pOT2.
Plasmid cDNA library."
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BI620499 555 bp mRNA linear EST 07-SEP-2001 RH51659.5prime RH Drosophila melanogaster normalized Head pFlc-1 Drosophila melanogaster cDNA clone RH51659 5, mRNA sequence.
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Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 565)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Carlson, M., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanenavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and
                                                                                                                                                   370 AGCAGCCCGAGGGGTTTATCTATATAGATGTCGCAGCTTATCATCTCATGCTGTGA 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RH Drosophila melanogaster normalized Head
pFlc-1"
                                                                                                                                                                                                                                                                                                                    541 ATCATCATCGGCGTCATTATCAACAGAATCAGCATCAGCATTTGGAGGCCCCGGTTGCTC
                                                                                                                                                                                                                                     430 GGTTGTTCTGTGTGCTCGTGTAGTATCTTAAATACATAGAGTGTGTTCATATAAAGTGCG
                                                                                                                                                                                                                                                               GGTTGTTCTGTGTGGTTAGTATCTTAAATACATAGAGTGTGTTCATATAAAGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                          550 ATCATCATCGTCGTCATTATCAACAGAATCAGCATCAGCATCTGGAGGCCCCGGTTGCTC
                                                                  310 AGAGAAAAACCAGTAGACAAAACAAGTGTGGTAATACAATCTGAAAAGGGCACCATC
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
hit genomic AE003831: arm:2R [4876906,5137815]
Plate: RK.516 row: E column: 11
High quality sequence scop: 442.
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/mol type="mRNA"
/db xref="taxon;7227"
/clone="RH51659"
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/lab_host="DH5-alpha TonA"
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BDGP/HHMI RH Drosophila EST Project
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Contact: Stapleton, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clome_lib="LP Drosophila melanogaster larval-early pupal
pOT2"
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LP03784.5prime LP Drosophila melanogaster larval-early pupal pOT2
Drosophila melanogaster cDNA clone LP03784 5prime, mRNA sequence.
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Drosophila melanogaster
Drosophila melanogaster
Brusryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 604)
Lewis, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.

BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: whole body; Vector: pOT2; Site 1: EcoR1; Site_2: Xho1; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library.
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 466 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence DS05033
Plate: 37 row: G column: 12
High quality sequence stop: 421.
High quality sequence stop: 421.
1. 604
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|mol_type="mRNA"
|db_xref="taxon:7227"
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/lab_host="DH5-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'clone="LP03784"
'sex="male and female"
                                                                                                                                                                                                                                                                                                AI260099.1 GI:3867624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Stapleton, M.
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Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a Xhol site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic AE003831: arm:2R [4876906,5137815]
pestimated-cyto:46B13-46E4: 02/08/2002
Plate: SD.182 row: H column: 2
High quality sequence stop: 456.
Location/Qualifiers
1. :508
/organism="Droscophila melanogaster"
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                                                                                                                                                                                                                                                                                                                     /mol_type="moreover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-recover-re
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                                                                                                                                                                                                                                                                                                                                                               124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCATCAGCAGCCCCAGGGGTTTATCTATATAGATGTCGCAGCTTATCATCTCATGCTGTC 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAACTAGAAAATATCTTGAGAAACTTGTTTTCGCGCTTTTTCTTTTGCTAATTGCCGATC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGGAAGAGAAAAACAAGCAGTAGACAAAACAAGTGTGGTAATACAATCTGAAAAGGGCA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTGAGGTTGTTCTGTGTGCTCGTGTAGTATCTTAAATACATAGAGTGTGTTCATATAAA 498
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RIKEN. The library was normalized and excised using recombinase. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.

(bases 1 to 508)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                   CGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCCGTTTCAGTTAACTACTACCAAG
                                                                                                                                                                                                                                  ATTGAATTTCGCCATCGGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACTGTGT
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                                                                                                                          565;
                                                                                                                          Length
                                                                                                                                                                              1; Indels
                                                                                                                    25.4%; Score 545.4; DB 12; 99.8%; Pred. No. 6.8e-59; ive 0; Mismatches 1;
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One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
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Unpublished (2001)
Other_ESTs: SD18286.5prime
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Contact: Stapleton, M.
BDGP
                                                                                                                    Query Match 25.4
Best Local Similarity 99.8
Matches 546; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565
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CK135985/c
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1902

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1962

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2082

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2023

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23

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BIG36564 linear EST 10-SEP-2001 SD18286.5prime SD Drosophila melanogaster Schneider L2 cell culture pCT2 Drosophila melanogaster CDNA clone SD18286 5 similar to CG12919: FBan0012919 GO:[] located on: 2R 46E1-46E1;: 05/19/2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          991 GACGACGATGGCGATGGATTCCATTGCGGACGACGACGACGACGACGACGTAGCTAT 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH5-alpha"
/clone_lib="SD Drosophila melanogaster Schneider L2 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                172 GTTCGTAGTACCTAGTCTTAGTCACTCCAAACCTAATCGGAATCGGAATCGCATACTG
                                                                                                                      112 CATTAGTCAGAAGACGGAGGAAAATCATATTTATGTTGTTGTATATACTCCTTCGACTCTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    931 TACGAGAATGCCCTCATCGACTATCCAAAAAGGTGGATGGCCTCACGGATGAGGAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
estimated-cyto:46B13-46B4: 05/19/2001
Plate: SD.182 row: H column: 2
High quality sequence stop: 491.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bobytera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pOT2; Site 1: EcoR1; Site 2: Xho1; ifractionated cDNAs were dTrectly ligated into pOT2 Plasmid cDNA library."
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    495
/organism="Drosophila melanogaster"

                                                                                                                                                                                     2084 AAGTGAATAAAATATATGTAGCTATTA 2111
                                                                                                                                                                                                                               25
                                                                                                                                                                                                                 52 AAGTGAATAAAATATATGTAGCTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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Matches 489;
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                                                                                                                                                                                                                                                                                                                                                                               Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: $10 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic AE003831 arm:2R [4876906,5137815]
estimated-cyto:46B13-46B4: 08/05/2002
Plate: RH.516 row: E column: 11
High quality sequence stope: 382.
Location/Qualifiers
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopeerygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (basea I to 532)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Garlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,
Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fnote="Organ: head, Vector: pFlc1; Site_1: XhoI; Site_2: BamHI, Library was Kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using cre recomblinase. Plasmid oDNA library."
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pFlc-1"
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/organism="Drosophila melanogaster"
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99.0%; Pred. No. 3.2e-53;
iive 0; Mismatches 5;
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/dev stage="Adult"
/lab_host="DH5-alpha TonA"
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                     Other ESTs: RH51659.5prime
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="RH51659"
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BX560278 Glossina morsitans morsitans adult infected gut Glossina morsitans cDNA clone T8e49al0_plc, mRNA sequence.
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1 (bases 1 to 612)
1 Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Iehane, M.J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
  83
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All clones with suffix qlc are reverse primer reads starting at end of the cDNA all plc reads are from the 3, end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 CCATCAGCAGCCCGAGGGTTTATCTATATAGATGTCGCAGCTTATCATCTCATGCTGTC
84 CGCGTGCGTGCATGATAGCGAAGAAAAAAGCTATCCGTTTCAGTTAACTACTTACCAAG
                                                                                                                                   125 ATTGAATTTCGCCATCGGGCAAATTACTAAAATACATAAGTGCAACTCGTCCACTGTGT
                                                                                                                                                             204 GTTGTG--TTTTTTTTTTTTTTTGCTGTGCCTTTATCGCAAACAAGAACTGAT
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 18A, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
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/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse49a10_plc"
/tissue_type="adult infected gut"
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Genome Biol. 4 (10), R63 (2003)
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       AACAATGCACATACCGGCACCACGCCCACATCTGAGACCACTGCTGAGGGCGAGGCGAG
                                                                                           1171 ACGGACAGTGCATCCTCAGCCTCAAATGATGACAATGTGTTCGATGACTTTACCAGCTAC 1230
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/clone_lib="SD Drosophila melanogaster Schneider L2 cell
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                            ACGGACAGTGCATCCTCAGCCTCAAATGATGATGATGTGTTCGATGACTTTACCAGCTAC
                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Edopter-rygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 447)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
estimated-cyto:46B13-46E4: 05/19/2001
Plate: SD.175 row: D column: 9
High quality sequence stop: 445.
Location/Qualifiers
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fractionated cDNAs were directly ligated into pOT2.
Plasmid cDNA library."
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/mol_type="mRNA"
/db_xref="taxon:7227"
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN37D20 of DrosBAC library from Drosophila melanogaster (fruit
                                        /note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
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                                                                                                                                                                                                                                                                          1631 ACAACTCGCACGACCAGAACGGATTTATCGTCTTTCAAGGAGACACTCCCATTCCTGCAGT 1690
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                     607 ATGGTGTCTTGACTATTCGCGAATCGGGTCTTTATTATGTTTATGCTCAAGTATGTTATA 548
                                                                                                                                                                                                                                                                                                                                                                                487 GCTTTCAAACTGTACCCACTAACATGTCACTGAAAATCCACTTGTCATACGAGCGGTT 428
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/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                               1571 ATGGCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCCAGATATGCTACA
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                                                                                                                                                              Gapa
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                     Length 612;
                                                                                                                   Score 129.8; DB 13; Length
Pred. No. 3.9e-07;
0; Mismatches 107; Indels
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/db_xref="taxon:7227"
/clone="BACN37D20"
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/plasmid="pBeloBAC11"
/note="end : T7"
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                                                                                                                     6.0%;
                                                                                                                                      Best Local Similarity 64.5
Matches 194; Conservative
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JOURNAL
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:4203736"
/dev_stage="embryo, stage 31-32"
/dev_stage="embryo, stage 31-32"
/dev_stage="embryo, stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage stage
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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1 (bases 1 to 468)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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     DB 29; Length 1101;
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                                                    ; Pred. No. 1.5e-05; 13; Mismatches 38
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48.9%; Pred. No. 47;
5.4%; Score 115.6; 72.0%; Pred. No. 1.5
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Location/Qualifiers
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Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Drs. Donald Brown and Liquan Cai

CDNA Library Preparation: CLONTECH

CDNA Library Preparation: CLONTECH

CDNA Library Preparation: CLONTECH

CDNA Library Preparation: CLONTECH

CDNA Gistribution: NGI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

http://image.llni.gov

Plate: LLCM3263 row: n column: 20

High quality sequence stop: 496.

Location/Qualifiers

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AGENCOURT 14011375 NICHD XGC Tadl Xenopus laevis cDNA clone
MAGE:6339285 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1099 TTAAATAAACTCAACAATGCACATACCGGCACCACGCCCACATCTGAGACCACTGCTGAG 1158
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                                                                                                                                                                                                                                       141 GATGATGATAAAGACGATGATGACGATGATGACGACGACGATGATGACGACGATGATGA
                                                                                                                                                                                                                                                                                                                                                                                                GACGACGACGATGATGATGATGATGATGTAAAAAAGGATGACGACGACGAT 260
                                                                              81 GATGATGACGACGATGATGATGATGACGACGATGATAAAGATGATGATGACGACGAC 140
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919 ITCCAAAAGGAGTACGAGAATGCCCTCATCGACTATCCAAAAAAGGTGGATGGCCTCACG 978
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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1 (bases 1 to 752)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                            GATGAGGAGGACGACGATGCTGCATCGCATTCCATTGCGGACGACGACGACGACGAC
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/db_xref="taxon:8355"
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Best Local Similarity 56.9
Matches 115; Conservative
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AUTHORS
TITLE
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                                                                                                                                                             447 GATAAAGACGATGATGACGACGATGATGATGACGACGACGATGACGATGACGAT 506
                                                                                                                                                                                                                                                                                         954
895 AACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCGACTAT
                                                       387 AATGATGACGACGATGATGACGACGATGATAAAGATGATGATGACGACGACGACGATGAT
                                                                                                                         955 CCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGCGATGGTCTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: September 15, 2004, 02:17:46
Job time : 8244 secs
                                                                                                                                                                                                                                                                                                                                                                           1075 GACTACGAGGACTACACCGATA 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                  567 GACGACGATGACGACGATGACA
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WPI; 2002-195121/25.
N-PSDB; ABK11680.
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(BOWE/)
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                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                               Aau 77716 Drosophil
Abb67553 Drosophil
Aau 88008 Tumour ne
Aau 88018 Tumour ne
Abg32871 Mouse Zis
Abg3245 C. albica
Aab 818165 Plasmodiu
Abb67073 Drosophil
Abb67173 Drosophil
Abb67173 Drosophil
Abb65698 Drosophil
Abb65698 Prosophil
Aau 86946 Human neo
Abb22760 Protein s
Abb681812 Prosophil
Abb64814 Drosophil
Abb64814 Drosophil
Abb64814 Drosophil
Abb63104 Human ech
Abb09082 Human ech
Abb09082 Human EDA
Abo01928 Human EDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aau77718 Drosophil
Aau77717 Drosophil
                                                                                        2; Search time 57 Seconds (without alignments)
2027.402 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                  US-09-813-329-6
2162
1 MTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters
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                                                                                        September 13, 2004, 10:21:32
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Listing first 45 summaries
                                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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        Frog zinc

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        RRP3 telo

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        128
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        6 AAE33788
        Human nuc

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        128
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        111
        4 AAU37362
        Aau37362
        Buman nuc

        31
        127.5
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        1111
        4 AAU37362
        Aau37362
        Braphyloc

        31
        127.5
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        164
        4 AAU15058
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        Protein e

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        Abb588581
        Drosophil

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        6 ABN71209
        Abb588581
        Drosophil

        35
        126.5
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        1274
        6 ABN71209
        Abb588581
        Drosophil

        36
        126.5
        5.9
        1274
        6 ABN71209
        Abb588581
        Drocophil

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ALIGNMENTS

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Tumour necrosis factor; TNP; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder; sparse hair; sweat gland aberration; endotoxic shock; inflammation; haemorrhagic necrosis of tumour; cytotoxicity; TNFv2; obesity-linked insulin resistance.
                                                                                                                              Drosophila melanogaster tumour necrosis factor variant 2 (TNFv2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bowen MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guan B,
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                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .52
/label=_Signal_peptide
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      Ź
AAU77718 standard; protein; 409
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                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                             Orosophila melanogaster.
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RAMANATHAN C
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GUAN B.
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                                                                                    05-JUN-2002
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New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm
                                                                                                                                                                                                                           Claim 6; Fig 3A-C; 119pp; English
                                                                                                                                       animals
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The invention describes an isolated tumour necrosis factor polypeptide

(TNF). The polypeptide and polynucleotide are useful in controlling
agriculturally important pests, particularly by modifying the growth,
feeding and/or reproduction of crop-damaging insects or insects of farm
animals. The polypeptide and polynucleotide are useful for modulating
cepithehial morphogenesis, cell-matrix adhesion in flies and mammals. Thus
the polypeptide and polynucleotide may be useful for treating,
ameliorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal
dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal
ike disorders, e.g. sparse hair, abnormal or missing teeth or sweat
like disorders, e.g. sparse hair, abnormal or missing teeth or sweat
cland aberrations in animals (e.g. insects and potentially humans),
endotoxic shock, inflammation, haemorrhagic necrosis of tumours,
cytotoxicity and obesity-linked insulin resistance, all of which involve
TNF molecules. This is the amino acid sequence of the Drosophila
melanogaster tumour necrosis factor variant 2 protein, described in the invention

Sequence 409 AA;

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                                                                                                       TTRVSHLDKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYENALIDYPKKVDGLTDEEDD 120
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                                       Gaps
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             Length 409;
                                    Indels
            Score 2162; DB 5;
Pred. No. 7.1e-182;
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100.0%; Scor.
100.0%; Pred. No. /...
0; Mismatches
                      Local Similarity 100.
             Query Match
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                                                                        Sequence 406 AA;
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                                                                                                                                                                                                                                                                                                                     Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder;
                                                                                                                                                                                                                                                                             Drosophila melanogaster tumour necrosis factor variant 1 (TNFv1)
361 MPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV
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                                                                                                                                 AAU77717 standard; protein; 406
                                                                                                                                                                                                                                (first entry)
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AAU77117;

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The invention describes an isolated tumour necrosis factor polypeptide

(TNF). The polypeptide and polynucleotide are useful in controlling
agriculturally important peets, particularly by modifying the growth,
feeding and/or reproduction of crop-damaging insects or insects of farm
animals. The polypeptide and polynucleotide are useful for modulating
cepithelial morphogenesis, cell-matrix adhesion in files and mammals. Thus
the polypeptide and polynucleotide may be useful for reating,
ameliorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal
dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal
dysplasia.

Inke disorders, e.g. sparse hair, abnormal or missing teeth or sweat
gland aberrations in animals (e.g. insects and potentially humans),
endotoxic shock, inflammation, haemorrhagic necrosis of tumnours,
cytotoxicity and obesity-linked insulin resistance, all of which involve
TNF molecules. This is the amino acid sequence of the Drosophila
melanogaster tumour necrosis factor variant 1 protein, described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                            1.52
| Jabel= Signal_peptide
53.0406 mature_TNF
| / Jabel= mature_TNF
| / Jote= "Tumour_necrosis factor. Specifically claimed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm
    shock; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bowen MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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Pred. No. 7.3e-175;
0; Mismatches 0;
    endotoxic
hair; sweat gland aberration; endotoxic rhagic necrosis of tumour; cytotoxicity;
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                                                                                               Location/Qualifiers
                                obesity-linked insulin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Fig 2A-B; 119pp; English.
                                                                                                                                                                                                                                                                                    20-MAR-2001; 2001US-00813329.
                                                                                                                                                                                                                                                                                                                  21-MAR-2000; 2000US-0190816P.
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96.4%;
                                                                                                                                                                                         claim 35"
                                                              Drosophila melanogaster
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RAMANATHAN C
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GUAN B.
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                haemorrhagic
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                                                                                                                                            Protein
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    sparse
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                                                                                                                                                                                                                                                                                                                                                                                                 XIAO/)
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                                                                                                                                                                                                                                                                                                                                                                                                            (GUAN/)
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Claim 6; Fig 1A-C; 119pp; English.
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                                                                                                                                                   Sequence 409 AA;
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294
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                                                                                                                                                                                                                                                                                                                                                              53. .409
/label mature_TNF
/note= "Tumour_necrosis factor. Specifically claimed in
                                                                                                                                                                                                                                                 Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder; sparse hair; sweat gland aberration; endotoxic shock; inflammation; haemorrhagic necrosis of tumour; cytotoxicity;
                                 DSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEATS
                                                         KESPAPLHHRRRMHSRHRHLLVRK-----ARSEDSRPAAHFHLSSRRRHQGSMGYHGDM
                                                                   ||------RMHSRHRHLLVRKGESLLSARSEDSRPAAHFHLSRRRHQGSMGYHGDM
                                                                                         YIGNDNERNSYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCL
                                                                                                  YIGNDNERNSYĞGHEQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVEQGBTPFLQCL
                                                                                                                          409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Drosophila tumor necrosis factor molecule, useful in controlling degriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm animals.
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                                                                                                                                                                                                                                   Drosophila melanogaster tumour necrosis factor (TNF).
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                                                                                                                                                                                                                                                                                                                                           1. .52
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ramanathan CS,
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                  AAU77716 standard; protein; 409 AA
                                                                                                                                                                                                                                                                                                   obesity-linked insulin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2000; 2000US-0190816P.
                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-2001; 2001US-00813329
                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    claim 34"
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                                                                                                                                                                                                                                                                                                                   melanogaster.
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RAMANATHAN C S
XIAO H.
GUAN B.
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N-PSDB; ABK11678.
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(RAMA/)
(XIAO/)
(GUAN/)
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                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARR/)
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agriculturally important pests, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polynucleotide are useful for modulating epithelial morphogenesis, cell-matrix adhesion in files and mammals. Thus polypeptide and polynucleotide are useful for modulating the polypeptide and polynucleotide may be useful for treating, ameliorating or preventing x-linked anhidrotic (hypohidrotic) ectodermal dysplasia and x-linked anhidrotic (hypohidrotic) ectodermal dysplasia and x-linked anhidrotic (hypohidrotic) ectodermal gland aberrations in animals (e.g. insects and potentially humans), endotoxic shock, inflammantion, haemorrhagic necrosis of tumours, cytotoxicity and obesity-linked insulin resistance, all of which involve TNF molecules. This is the amino acid sequence of the Drosophila melanogaster tumour necrosis factor protein, described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 KESPAALHLRRRMHSRHRHLVVRKARSEDSRPAAHFHLSSRRRHQESMGYHGDMYIENDR 300
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invention describes an isolated tumour necrosis factor polypeptide ). The polypeptide and polynucleotide are useful in controlling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSASSASNDDNVFDDFTSSDALKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MTAETLKPFITPTSANDDGFPAKATSTATAQRRTRQLIPLVLGFIGLGLVVAILALTIWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2045; DB 5;
Pred. No. 1.5e-171;
2; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.3'
Matches 394; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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AAU88018 standard; peptide; 27
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                                                 Drosophila melanogaster,
                                                                                                                                                                                                                                               Chen J,
                                                                                                                                                                             CHEN J.
RAMANATHAN C
                                                                                                                                                                   CARROLL P M.
                                                                                                                                                                                                                                                                      WPI; 2002-195121/25
                                                                                                                                                                                                                           BOWEN M A.
                                                                                                                                                                                                   XIAO H.
GUAN B.
                                                                       US2002012968-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27 AA;
                                                                                                                                                                                                                                                 Carroll PM,
                                                                                               31-JAN-2002
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                                                                                                                                                                                                    (XIAO/)
                                                                                                                                                                              (CHEN/
                                                                                                                                                                                          (RAMA/
                                                                                                                                                                                                               (GUAN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 NNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRN 308
                                                                                                                                                                                                                                                                                                                                                                                                            9 QYENALIDYPKKVDGLTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMINK 68
                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therepeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), axpressed DNA ABR72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAHFHLSSRRRHQGSMGYHGDMYIGNDNERNSYQGHFQTRDGVLTVTNTGLYYVYAQICY
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                                                                                                                                                                      Disclosure; SEQ ID NO 29451; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                   Length 325;
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                                                                                                                                                                                                                                                                                                                                                Score 1656; DB 4;
Pred. No. 2.2e-137;
1; Mismatches 0;
                                                                     Myers EW;
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                                                                   PWD,
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          23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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97.8%;
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Matches 310; Conservative
                                                                  Adams M,
                                                                                         2001-656860/75.
                                            (PEKE ) PE CORP NY.
                                                                                                    N-PSDB; ABL11656
                                                                                                                                                                                                                                                                                                                           Sequence 325 AA;
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                                                                 Venter JC,
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The invention describes an isolated tumour necrosis factor polypeptide (TNF). The polypeptide and polynucleotide are useful in controlling agriculturally important pests, particularly by modifying the growth, electing and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polynucleotide are useful for modulating capturalized and polynucleotide are useful for modulating the polypeptide and polynucleotide are useful for reating. Thus the polypeptide and polynucleotide may be useful for treating. Thus the polypeptide and polynucleotide may be useful for treating. Thus the polypeptide and polynucleotide may be useful for treating. Thus the polypeptide and polynucleotide may be useful for treating. Thus the polypeptide and polynucleotide may be useful for treating. Thus the polypeptide and polynucleotide may be useful for treating. Cytotocaic and x-linked animidatotic (hypohidrotic) ectodermal dysplasia-like disorders, especially humans), endocatic and obesity-linked insulin resistance, all of which involve TNF molecules. This sequence represents a tumour necrosis factor peptide useful as an antigenic epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm
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               endotoxic shock; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowen MA;
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100.0%; Pred. No. 5.4e-06;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guan B,
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sparse hair; sweat gland aberration; endotoxic haemorrhagic necrosis of tumour; cytotoxicity; obesity-linked insulin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ramanathan CS, Xiao H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 TRDGVLTVTNTGLYYVYAQICYNNSHD 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 22; 119pp; English.
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Parkinson's disease, Alzheimer's disease, neurodegenerative disease,
zinc finger splicing with extended Ser-Arg domain, secretory pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm animals.
sparse hair; sweat gland aberration; endotoxic shock; inflammation;
haemorrhagic necrosis of tumour; cytotoxicity;
obesity-linked insulin resistance.
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100.0%; Pred. No. 5.4e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ramanathan CS, Xiao H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TRDGVLTVTNTGLYYVYAQICYNNSHD 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 98; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG32871 standard; protein; 330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful as an antigenic epitope
                                                                                                                                                                                                                                                                                                              21-MAR-2000; 2000US-0190816P.
                                                                                                                                                                                                                                                           20-MAR-2001; 2001US-00813329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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168 27; Conservative
                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                             CHEN J.
RAMANATHAN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Zis-SR protein.
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                                                                                                                                                                                                                                                                                                                                                                  CARROLL P M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-195121/25
                                                                                                                                                                                                                                                                                                                                                                                                                                     (XIAO/) XIAO H.
(GUAN/) GUAN B.
(BOWE/) BOWEN M A.
                                                                                                                                                    US2002012968-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carroll PM,
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The invention relates to an isolated nucleic acid molecule, Zis-SR, encoding a protein involved in the secretory pathway in a cell ( or its homologue or variant) or nucleic acid molecules that hybridise under high stringency condition to the Zis-SR nucleic acid. Also included are an isolated polypeptide involved in the formation of secretory granules in cells comprising the amino acid sequence spanning amino acids 243-310 of the Zis-SR protein, restoring the neuroendocrine differentiation of a cell using the nucleic acid molecule or polypeptide cited above, independentlying a gene and/or protein involved in inducing regulated secretion-defective cell line under conditions that restore differentiation of the secretion-defective cell, such that secretion is restored, and the secretion-defective cell, such that secretion is restored, and the secretion-defective cell, such that secretion is restored, and the secretion candulating the secretion in a cell comprising and an assay to identify a modulating the secretion in a cell comprising and a sessesment of a biological activity of Zis-SR, its part or derivative in the presence of a candidate agent, where a modulation of regulated secretion is selected when the biological activity of Zis-SR, its part or derivative is measurably different in the presence of the candidate or complated are useful for regulating neuroendocrine phenotype, and for properties of a cell, for regulating neuroendocrine phenotype, and for properties of a cell, for regulating neuroendocrine phenotype, and for long term thearapies to treat diseases or conditions associated with a loss of function, e.g. disbetes, neurodegenerative diseases such as a loss of function, e.g. disbetes, neurodegenerative diseases such as longered per expresence of polypeptides are useful for regulating diseases. The assay is useful for defect in the regulated secretory abhways in cells. The nucleic acid molecules can also be used to locate gene regions associated with a defect in the present sequence represents mountse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Zis-SR nucleic acid molecules and polypeptides, useful for restoring or increasing the secretory properties of a cell, or for treating diseases or conditions associated with a loss of function, e.g. diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 FARRTSCNRCGREKTTEAKMMKAGGTEIGKTLAEKSRGLFSANDWQCKTCSNVNWARRSE 84
                                                                                  /note= "This region is specifically claimed in claim 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPAKATSTATAQRRTRQLIPLVLGFIGLGLVVA----ILALTIWQTTRVSHLDKELKSL
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                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Fig 4; 70pp; English.
                                                                                                                                                                                                                                                            29-JAN-2001; 2001US-0264296P.
                                                                                                                                                                                                                   29-JAN-2002; 2002WO-CA000101
                                                                                                                                                                                                                                                                                                        (UYSH ) UNIV SHERBROOKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkinson's disease.
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Best Local Similarity
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144 ILKEVEDKESEGEEEDEDEDELSKYKLDEDEDEDDADLSKYNLDASEEEDSNKKKSNRRSR 203
                                                                                204 SKSRSSHSRSSSRSRSRSRSRSRSRSRSRSRSSSSSQSR---SHSGSREHSRGRGSKSRS-- 258
                                                                                                                     DVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSR-PA 273
                                                                                                                                                ----SSRSHRGSSSPRKRSYSSSSS----PERDRKRSRSRPSSPAVRKKRTRSRSPE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preparing a medicament for treating, preventing and/or alleviating diseases associated with yeast or fungi or proliferative disorders, such as cancer, or for preventing apoptosis in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for
          V-----DGLTDEEDDDDGDGLDSIADDEDDVSYSSVDDVGADYEDYTDMLNKLNN---- 161
                                                                                                                                                                                                                                                                                                                                                                                    Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide; vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel nucleic acid representing a synthetic least gene. The Bax gene of the invention is useful for identifying Baxresistant yeast or fungi, identifying, or obtaining and identifying Candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax induced cell death. The products of the invention have cytostatic, fungicide; immunosuppressive, virucide and vasocropic activity and can be used in vaccines or for gene therapy. The isolated nucleic acids, polypeptides, pharmaceutical compositions, antisense molecules and antibodies are useful as medicaments or in
                                                              -----AHTGTTPTSETTAEGEGETDŞASSASNDDNVFDDFTSYNAHKKKQERKSRSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid representing a synthetic BAX-gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                                                           C. albicans BAX-associated protein fragment SEQ ID 448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reekmans RJ;
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                                                                                                                                                                                                                                                                          ABG93245 standard; protein; 428 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-2000; 2000EP-00870318.
04-JAN-2001; 2001EP-00870002.
09-JAN-2001; 2001EP-00870003.
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                                                                                                                                                                           274 AHFHLSSRRRHQGS 287
                                                                                                                                                                                                                                                                                                                                (first entry)
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preparing a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease, ischaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polypeptide associated with the Bax gene described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 DDVSYSSVD-DVGADYEDYTDMLN-KLNNAHTGTTPTSETTAEGEGETDSASSASNDDNV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 FDDFTSYNAHKKKQERKSRSIADVRNE---EQNIQGNHTEL---QEKSSNEATSKESPAP 246
                                                                                                                                                                                                                                                                                                                                                                                                66 ÓLLPIAKMSSNTODLVLAYINDYVSRNEELSKLKKALSKFLAGKELPKVSKOLESIIDEV 125
                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 PEDKKRKHTDDIKEEKPVKKFKNESESSASSSTDSIPATPEPELKPGQRKHFSRIDRSKV
                                                                                                                                                                                                                                                                                                                                                  -----KSLKRVVDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 QQR----LGINYLDEFDEFQKEYENALIDYPKK---VDGLTDEEDDDDGDGLDSIADDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 ENQEKKSKPRNSSSDSEDSSSESESSTSDSESSSSDSDSSSSDSESSSSDSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 LHHRRRMHSR--HRHLLVRKARSE------DSRPAA------HFHLSSRRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------HQGSMGYHGDM------YIGNDN--ERNSYQGHFQTRDGVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 NFENSVLODNTYKGAAGTWGEKASEKLLOVRGKDFTKNKNKMKRGSYKG-----GSITL
                                                                                                                                                                                                                                                                                             84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 2; human malaria parasite; vaccine; protozoacide; infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum chromosome 2 related protein SEQ ID NO:22
                                                                                                                                                                                                                                            Length 428;
                                                                                                                                                                                                                                         6.5%; Score 141; DB 5; Length 42
0.8%; Pred. No. 0.0015;
ve 68; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                            36 QLIPLV-LGFIGLGLVVAILALTIWQTTRVSHLDKEL---
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Best Local Similarity 20.00,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 TNTGLY 324
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CARUCCI D.
GARDNER M.
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                                                                                                                                                                                        Sequence 428 AA;
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by chromosome 2 of the human malarial parasite, plasmodium falciparum. Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II): (I) and polyclonal antisers or a monoclonal antibody raised to imfection. (I) and polyclonal antisers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Farthermore, (I) (sepecially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum. Sequencing of the coldentify drug resistance in P. falciparum. Sequencing of the coldentify drug resistance in P. falciparum. Sequencing of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 crepresent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYENAL----IDYPKKVDGLTDEE---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|| : |: :: | :| || || EKETEVEKKTEKDEE--GTDYEEDTDDSDKDVETEVEETDAEDKEENEEGTDDEEDKVE 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           773 ООУЕРУХИРЬЕООМУОТНН-----ІТКОООМУНРИНІТКОООМНИРНІГОЕОЕКНИР 825
                                                                                                                                                   and their fragments (I) encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 GDTPFLQCLNTVP----TNMPHKVHTCHT-----SGLIHLERNERIHLKDIHND 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                    encoded by chromosome 2 of the human malarial parasite, im falciparum, useful as antimalarial vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila, developmental biology, cell signalling, insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.4%; Score 138.5; DB 3; Length : 20.4%; Pred. No. 0.011; tive 60; Mismatches 145; Indels
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                                                                                                                                                present invention describes proteins
                                                                                                        Disclosure; Page 60-63; 577pp; English
                                        Plasmodium falciparum, useful as anti
diagnosis of P.falciparum infection.
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Best Local Similarity
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA agquences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA-associated protein; RNAAP; human; clone 869138; cytostatic; immunosuppressive; antiinflammatory; keratolytic; neuroprotective; antiarteriosclerotic; hepatotropic; antippsoriatic; virucide; anti-HIV; antiallergic; antirheumatic; antiarthritic; opthalmological; autoimmune; antimicrobial; cell proliferative disorder; inflammation; cirrhosis;
                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 KVDGLTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNK-LNNAHTGTT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 1883;
                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 6906; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.4%; Score 138.5; DB 4;
24.5%; Pred. No. 0.021;
... Mismarches 77;
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11-JUL-2000; 2000US-00614150.
                                                                                                   23-MAR-2001; 2001WO-US009231
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Drosophila melanogaster.
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hes 52; Conserv
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                                 WO200171042-A2.
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actinic keratosis; bursitis; arteriosclerosis; artherosclerosis; hepatitis; myelofibrosis; primary thrombocythemia; psoriasis; cancer; mixed connective tissue disease; MCTD; HIV; uveitis; Crohn's disease; allergy; rheumatoid arthritis; parasitic infection.
                                                                                                  note= "Potential phosphorylation site"
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1abel= ATP/GTP_binding_site_motif_A
Trote= "P-loop"
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The present amino acid sequence is the human RNA-associated protein-8 (RNAAP-8), identified in Incyte clone 869138, derived from LUNGASTO1 library. It is expressed in reproductive, nervous, gastrointestinal and heematopoietic/immune tissues. It has cytostatic, immunosuppressive, antinflammatory, antiarteriosclerotic, hepatotropic, keratolytic, neuroprotective, antipsoriatic, anti-HIV, antiallergic, antirheumatic, virucide, antibodies are useful for diagnosis of diseases associated with altered expression or activity of RNAAP. It is used to treat cell proliferative, autoimmune, inflammatory and infectious disorders, like actinic keratosis, bursitis, arteriosclerosis, artherosclerosis, cirrhosis, hepatitis, myelofibrosis, mixed connective tissue disease chematoid arthritis, uveitis, Crohn's disease, and bacterial, viral and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 KRVVD----NLQQRLG-----INYLD-----EFDEFQKEYENALIDYPKKVDG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204
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                                                                                                                                                                                                                                                                    Human RNA-associated proteins useful in diagnosing, treating and preventing cell proliferative, autoimmune, inflammatory and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 FARRISCNRCGREKTTEAKMMKAGGTEIGKTLAEKSRGLFSANDWQCKTCSNVNWARRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 ---LTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 FPAKATSTATAQRRIRQLIPLVLGFIGLGLVVA----ILALTIWQTTRVSHLDKELKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 QEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARS-----EDSRPAAHFHLSSRRRHQ
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                                                                                                                                                          GA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.3%; Score 137; DB 3; Length 33
21.2%; Pred. No. 0.0023;
Eve 49; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 PASILKEVEDKESEGEE---EDEDEDLSKYKLD-------
                                                                                                                                                        Yue H, Tang YT, Corley NC, Guegler KJ,
Baughn MR, Lal P, Bandman O, Reddy R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 85-86; 123pp; English.
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GSSSPRKRSYSSSSSSPERN 284
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                                              99WO-US019361
                                                                            98US-0097550P
99US-0115639P
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                                                                                                                                                                          Patterson C, Baughn MR, I
Shih LL, Yang J, Lu DAM;
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es 68; Conservative
                                                                                                                         (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                       WPI; 2000-237651/20.
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                                              20-AUG-1999;
                                                                          21-AUG-1998
              02-MAR-2000
                                                                                                                                                          Hillman JL,
                                                                                                                                                                                                                                                                                                   disorders.
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ABB67173 standard; protein; 532 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175 and the encoded proteins (ABB27137-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pt_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEEDDDDGDGLDSIADDEDDDVSYSSVDD-----VGADYEDYTDMLNKLNNA-----HTG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----NVFDDF 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 DEEDDDD------DDDDDDDEEEASTRGRSRRRNGVAVSASSSGSNRVTSSSAAQQRRG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----RMHSRH-----RHLLVRKARSEDSR------PAAHFHLSSRRRHQGS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSSAEEAASHSQHDESTQDSQIGRRKGRSASSRSIGNGPSTSAAAAANSSLESPSRNTRA 381
                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 28311; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.3%; Score 137; DB 4; Length 532; 22.6%; Pred. No. 0.0046; ive 37; Mismatches 93; Indels
                                                            Drosophila melanogaster polypeptide SEQ ID NO 28311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGYHGDMYIGNDNERNSYQGHFQTRDGVLTVTNT 321
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                                                                                                                                                                                                                                                                                                                                                Myers EW;
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                                                                                                                                                                                                                                                                23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                             (first entry)
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                                                                                                                                       Drosophila melanogaster.
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                                                                                                                                                                    WO200171042-A2
                                                                                                          pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions.
                                                                                                                                                                                                                                 23-MAR-2001;
                             26-MAR-2002
                                                                                                                                                                                                   27-SEP-2001
                                                                                                                                                                                                                                                                                                                                              Venter JC,
ABB67173;
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Best Local
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 PAKATSTATAQRRTRQLIPLVLGFIGLGLVVAILALTIWQTTRVSHLDKELKSLKRVVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAATVATGAAAAAAATPIATGNVKSGSTTSNANHT---NSNNSHQDEE------
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                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 23886
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21.8%; Pred. No. 0.035;
[ve 45; Mismatches 111;
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ABB65698 standard; protein; 2175 AA.
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11-JUL-2000; 2000US-00614150
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les 64; Conservative
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                                                                                                                                                                                                                                                                                        Drosophila melanogaster.
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N-PSDB; ABL09801
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                                                                                                                                                                                                          Drosophila;
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                                                    ABB65698;
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2000US-0249264P.
2000US-0249264P.
2000US-0249264P.
Human, neoplastic disease associated polypeptide; cancer; hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardicovascular disorder; neuroprotective; cardicovascular disorder; renal disorder; neuroprotective; cytostatic; anti inflammatory; vasotropic.
                                                                                          Novel human neoplastic disease associated polypeptide #261
                           AAU21828 standard; protein; 330 AA
                                                                                                                                                                                                                                                                     2000US-0180628P.
2000US-0180628P.
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autoimmune disease; human immundeficiency virus; timmune uncourt; annotoimmune disease; human immundeficiency virus; HIV; infection; anaemia; rheumatoid arthritis; multiple sclerosis; cancer; melanoma; hyperproliferative disorder; neurological disease; Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cerebrovascular disorder; angina; ocular disorder; corneal infection; wound healing; blorhythm transplantation; mesodermal tissue differentiation; embryonic stem cell; catabolism; anabolism; energy storage; mental state; hormone; appetite; reproductive potential; memory; stress; food additive;
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17-NOV-2000;
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The invention relates to novel isolated nucleic acid molecules (I)
encoding human secreted DNA repair and processing proteins (II). (I) and
concing human secreted DNA repair and processing proteins (II). (I) and (II) may be used in the prevention, treatment and
diagnosis of diseases associated with inappropriate expression of (II),
concerned of (II) may be used to treat disorders associated with
decreased expression of (II) by rectifying mutations or deletions in a
concerned may also be used as DNA probes in diagnostic assays (e.g.
concerned may also be used as DNA probes in diagnostic assays (e.g.
polymerase chain reactions (PCR) to detect and quantitate the presence
concerned may also be used as antigens in the production
concerned in samples, and so which patients may be in need of
restorative therapy. (II) may also be used as antigens in the production
concernibodies and in assays to identify modulators (agonists and
contibodies and in assays to identify modulators (agonists and
antibodies and in assays to identify modulators (agonists and
control of the expression and activity of (II). The anti-(II)
antibodies and antagonists may also be used to down regulate expression
and activity of (II). The anti-(II) antibodies may also be used as
concerned and antagonists may also be used to down regulate expression
and activity of (II). The anti-(II) antibodies may also be used to
disorders include e.g. immune/autoimmune diseases (e.g. human
confunctioned in the presence of (II) in samples. The
immunodeficiency virus (HIV), infections, anaemia, rheumatoid arthritis
confunctioned and thrombosial diseases (e.g. Alzheimer's disease and
confunctioned and thrombosis), infections caused by bacteria, viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 KRVVD-----NLOORLG------INYLD-----EFDEFOKEYENALIDYPKKVDG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules encoding human secreted DNA repair and processing proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 FARRTSCNRCGREKTTEARMMKAGGTEIGKTLAEKSRGLFSANDWQCKTCSNVNWARRSE 94
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21.2%; Pred. No. 0.0035;
.ive 48; Mismatches 108; Indels 96; Gaps
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                                                     2000US-0249218P
2000US-0249244P
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26, Appl
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US-08-431-080-28
US-08-33-534-28
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US-08-33-152A-29
US-08-007-999B-4
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US-09-105-343A-5
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; Sequence 2, Application US/09342681C
; Bacent No. 6355782
; GENERAL INFORMATION:
; APPLICANT: Zonana et al.
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
; CURRENT APPLICATION NUMBER: US/09/342,681C
; CURRENT FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: 60/102,279
; PRIOR FILING DATE: 1998-07-09
; PRIOR FILING DATE: 1998-1-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
                        Sequence 26, Appl
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US-08431-080-28
Sequence 28, Application US/08431080
Factor No. 569866
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                        US-09-345-294-26
US-09-531-029-90
US-08-128-123A-2
US-09-1298-568-2
US-09-410-399-2
US-09-620-093A-2
US-09-134-001C-5080
US-09-134-001C-5080
US-09-199-287B-19
US-09-588-947A-19
US-09-588-947A-19
US-09-588-947A-19
US-09-588-947A-19
US-09-588-947A-19
US-09-588-947A-19
US-09-186-656-014-2
US-09-386-937-10
US-09-386-937-10
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; Pred. No. 0.00046;
31; Mismatches 63;
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Best Local Similarity 28.6%;
Matches 44; Conservative 31
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CORGANISM: Homo sapiens
US-09-342-681C-2
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; TOPOLOGY:
US-08-938-534-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 DGSDSDSB-----TSSDDENIDFVKLTAQRKKRAMKALSAMNTNSNTLYSSRENSNK 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 NKSVKLSPKKENEEEQKEEKEKEKEEQQKQQESNKKEVNGSGTTTTQQALSFKFKKEDDG 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 NERN------SYQG--HFQTRDGVLTVTNTGLYYVYAQ-ICYNNSHDQNGFIVFQ 345
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19.9%; Pred. No. 0.0039;
tive 48; Mismatches 126; Indels 120; Gaps
                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/NS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,080
FILING DATE: Concurrently Herewith
CLASSIFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
ATORNEY/AGENT INPORMATION:
NAME: PARKEY, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/POCKET NUMBER: 32,165
REFERENCE/POCKET NUMBER: 32,165
REFERENCE/POCKET NUMBER: 32,165
RELEPHONE: (512) 418-3000
THELEPAR: (713) 789-2679
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                                                 UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                           TELERAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               1085 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 19.99
Matches 73; Conservative
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                             COMPUTER READABLE FORM:
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                   Houston
                                    TEXAS
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                                               COUNTRY:
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US-08-938-534-28
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Sequence 28, Application US/08938534 Patent No. 2916752 GENERAL INFORMATION: APPLICANT: Gottschling, Daniel E.

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69 KELKSIKRVVDNLQQRLGINYLDEFDEFQ-----KEYENALIDYPKKVDGLTDEEDDDDG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- GEGETDSASSASNDDNVFDDF 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 ------YDIDQDAYFDVINNEDSHGEIGTDLETGEDDLFILEE 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 APLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMGY-----HGDMYIGND
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APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  COMPUTER FEADBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,534
FILING DATE: 2c-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION: 636
PRIOR PRIOR PRIOR DATA:
APPLICATION: 636
FILING DATE: 08/431,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Parker, David L. REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
                                                              STREET: P.O. Box 4433
CITY: Houston
STATE: TEXA®
                                                                                                                                                      STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
SIR: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: OCCODER 20, 1994
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
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TELEFAX: (713) 789-2679
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STRANDEDNESS: siz
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CORDUTE: TENDED disk
CONDUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPETATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,152A
FILLNG DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTOREX/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36,688
ER: 0609.4120000
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TELECOMMUNICATION:
TELEPHONE: 202-371-2600
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SEQUENCE CHARACTERISTICS:
LENGTH: 706 amino acida
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346 GDTPFLQ 352
                                        417 FDMPFYE 423
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US-08-339-152A-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 NKSVKLSPKKENEEEQKEEKEKEKEEQQKQQESNKKEVNGSGTTTTQQALSFKFKKEDDG 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 ------YDIDQDAYFDVINNEDSHGEIGTDLETGEDDLFILEE 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 NERN-----SYQG--HFQTRDGVLTVTNTGLYYVYAQ-ICYNNSHDQNGFIVFQ 345
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                                   Sequence 28, Application US/09345294
Patent No. 6387619
GENERAL INFORMATION:
APPLICANT: Gottechling, Daniel E.
Singer, Mitiam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ANDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                           COUNTEY: UNITED STATES OF AMERICA

ZIP: 77210

COMPUTER READABLE FOORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: 105/09/345,294

FILING DATE: 30-Jun-1999
CLASSIFICATION: CURNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMUNICATION INFORMATION:
TELEFHONE: (512) 418-3000
TELEFFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/431,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino acids
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INFORMATION FOR SEQ ID NO: 28:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
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                    US-09-345-294-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-345-294-28
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US-08-007-999B-4

275 YXDTFK--GDDYNEE----NPTEPGSDGTMSDKEITHDVKVPPTPLPTNDVDVYFETSAD 328 91 DEFDEFQKEYENALIDY-----PKKVD------GLTDEEDDDGDGLDSIADDEDDDV 137 138 SYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTAEGE-----GETDSASSASND 189 ---KSRS 212 Sequence 29, Application US/08339152A
Patent No. 5643726
GENERAL INFORMATION:
APPLICANT: Crams, Dora M.
TITLE OF INVENTION: Methods For Modulating Transcription
TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
NUMBER OF ENQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Mashington 213 IADVRNEEQNIQGNHTELQEKSSNE-----ATSKESPAPLHHR------ 250 389 KAEAASEKOOLVETHLARVEAMLNDRRMALENYLAALORSDPRPHRILOPLRRYVRAEN 448 251 -RRMHS-RH-RHLLV---RKARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNERN 303 Gape 95; Length 706; Query Match 5.7%; Score 122.5; DB 1; Length Best Local Similarity 21.1%; Pred. No. 0.0084; Matches 63; Conservative 36; Mismatches 105; Indels

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APPLICANT: Wasco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Magendantz, Margaret
APPLICANT: Solomon, Frank
ITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
STRFFT
STRFFT
STRFFT
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COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,999B
FILING DATE: 21-JAN-1993
PRIOR APPLICATION NUMBER: US 07/872,642
FILING DATE: 10-ANG-1992
PRIOR APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-ANG-1992
ATTORNEY AGENT INFORMATION:
NAME: TOWNSEND, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 10609:3520002/JAG/GKT
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC COMPA
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Best Local Similarity
Matches 63; Conserva
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US-08-689-276A-4

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              GENERAL INFORMATION:
APPLICANT: Wasco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Bupp, Keith
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Solomon, Frank
APPLICANT: Solomon, Frank
APPLICANT: Solomon, Trank
ANTICID OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Pox P.L.L.C.
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STREET: 1100 New York Ave., NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06 - AUG-1996
FILING DATE: 06 - AUG-1996
FILING DATE: 06 - AUG-1996
FILING DATE: 06 - AUG-1996
FILING DATE: 10 - AUG-1996
FILING DATE: 10 - AUG-1993
FILING DATE: 20 - APR-1992
FILING DATE: 20 - APR-1992
FILING DATE: 20 - APR-1992
FILING DATE: 17 - AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 20 - APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 20 - APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: JORGE A. GOLDSTEIN
REGISTRATION NUMBER: 29 - 021
REFERENCE/DOCKET NUMBER: 29 - 021
REFERENCE/DOCKET NUMBER: 20 - 009 - 3520003
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 4, Application US/08689276A
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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158 KLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNA-----HKKKQER-- 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 KEYENALIDYPKKVDGLTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 KNGKNA-----KKEDSDEDEDDDDDDDDDDDDDDEDEED------EFEP----- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 PVVKGKQGKVAAAAPASEDEDEEEBEEEEBÜBEEEBÜSEEEBÄMEITPAKGKKAPAKVV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 --KSRSIADVRNEEQNIQGNHTELQEKSSNEATSKE-----SPAPLHHRRRMHSRHRH 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 122.5; DB 4; ilarity 20.0%; Pred. No. 0.0086; Conservative 40; Mismatches 109;
                                                                                                                                                                                                                                        HUMAN NUCLEOLIN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                         COUNTY NEW TOWN COMPACTER READABLE FORM:
MEDIUM TYPE: Diskette COMPACTER IBM COMPACTION COMPACTION COMPACTION COMPACTION COMPACTION CONTRAIN APPLICATION DATA:
APPLICATION NUMBER: US/09/241,333
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/990,114
FILING DATE:
ATTORNAY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: SETELEDHONE: 650-855.0555
                                                                                         336 DLAVVDVRTGTNRKFGYVDFESAED 360
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                                                                                                                                                                                                                                                                                                                STREET: 3174 Porter Drive
CITY: Palo Alto
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity
Matches 53; Conserva
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LIBRARY: GenBank
CLONE: 128842
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                                                                            US-09-241-333-3
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                                                                  Sequence 3, Application US/08990114
Patent No. 5932475
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Yue, Henry
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 122.5; DB 2;
20.0%; Pred. No. 0.0086;
tive 40; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskerte
COMPUTER: IBM Comparible
OPERATING SYSTEM: DOS
SOFTWARE: FastENG for Windows Version 2.0
CURENT APPLICATION NUMBER: US/08/990,114
FILING DATE: Herewith
                                                                                                                                                                                                                             STREET: JOYCE Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 76,749
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEFAX: 650-845-0555
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SEQUENCE CHARACTERISTICS:
LENGTH: 714 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity
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CLONE: 128842
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                                                   US-08-990-114-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 NAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRH 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 ETHSHKQSRLYKRKA---NDESN---EHSDVIDSQELSKVSRE----FHSHEFHS-HED 265
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22.8%; Pred. No. 0.003;
tive 30; Mismatches 78; Indels 99;
                          ACESULT 10
US-07-712-476A-1
Sequence 1, Application US/07712476A
Sequence 1, Application US/07712476A
Sequence 1, Application US/07712476A
STATLE OF INVENTION:
MUMBER OF INVENTION:
MUMBER OF SEQUENCES:
SCORRESPONDENCE ADDRESS:
MUMBER OF SEQUENCES:
STREET:
MUMBER OF SIQUENCES:
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2

SOFTWARE: WORDERFECT 5.0

SOFTWARE: WORDERFECT 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/712,476A

FILING DATE: 19910610

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: WILLIAM

ATTORNEY/AGENT INFORMATION:

NAME: SUZANDE E. MILLER

REGISTRATION NUMBER: 32,279

REFERENCE/DOCKET NUMBER: UPN 0473

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568 3100

TELEPHONE: (215) 568 3439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 296 amino acids
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336 DLAVVDVRTGTNRKFGYVDFESAED 360
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Best Local S
Matches 61
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RESULT 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 EETUDFKQE-----TLPSKSNESHDHMDDMDDEDDDDHVDSQDSIDSNDSDDTDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 PDIQYPDATDEDITSHMESEELNGAYKAIPVAQDLNAPSDWDSRGKDSYETSQLDD-QSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 ETHSHKQSRLYKRKA---NDESN---EHSDVIDSQELSKVSRE-----FHSHEFHS-HED
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Sequence 1, Application US/09134253
Fatent NO. 6509026
GENERAL INFORMATION:
TITLE OF INVENTION: Osteopontin Coated Surfaces and Methods of Use
TITLE OF INVENTION: Osteopontin Coated Surfaces and Methods of Use
TITLE OF INVENTION: Osteopontin Coated Surfaces and Methods of Use
CURRENT APPLICATION UNMER: US/09/134,253
CURRENT FILING DATE: 1998-08-14
EARLIER FILING DATE: 1998-08-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 DEFDEFQKEYENALIDYPKK------VDGLTDEEDDDDGDGLDSIADDEDDDV----S
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Patent No. 6551990
Patent No. 6551990
Patent No. 6551990
TIPORMATION:
APPLICANT: Steitz, Susie
TITLE OF INVENTION: Methods of Inhibiting Ectopic Calcification
FILE REFERENCE: P-UW 3244
CURRENT APPLICATION NUMBER: US/09/206,576
CURRENT FILING DATE: 1998-12-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.6%; Score 121.5; DB 4; Length 314; Best Local Similarity 22.8%; Pred. No. 0.0032; Matches 61; Conservative 30; Mismatches 78; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 YSSVDDVGADYED--YTDMLNKL--NNAHTGTTPTSETTAEGEGET----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 LLV -- RKARSEDSRPAAHFHLSSRRHQ 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-134-253-1
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ORGANISM: Homo sapiens
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203 KKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRHLLV 262
                                                                              103 ARRA-----IAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 VRKARSEDSRPAAHFHLSSRRRHQGSM-GYHGDMYIGNDNERNSYQG-HFQTRDGVLTVT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 NIGLYYVYAQICYNNSHDQNGFIVF----QGDIPFLQCLN----TVPTNMPHKVHTCH 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208 RKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKES--PAPLHHR----RRMHSRHRHLL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 RASLSAQEPAQEELVAE----EDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTR 102
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                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09105343A
; Sequence 2, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION;
; TITLE OF INVENTION: MEMBER OF THE TWF FAMILY USEFUL
; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDOCT Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park Road
; STATE: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.4%; Score 116; DB 3; Length 249; illarity 25.5%; Pred. No. 0.0075; Conservative 33; Mismatches 95; Indele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
OPETWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,343A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA;
APPLICATION NUMBER:
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INPORMATION:
NAME: BECKER, Cheryl L.
REGISTATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6048.US.P2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                             263 -- RKARSEDSRPAAHFHLSSRRHQ 285
                                                                                                                                                                                                    255 VDPKSKEEDK-----HLKFRISHE 273
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12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SILL.
COUNTRY: USA
ZIP: 6064-6050
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
"""ITTER: IBM Compatible
"""ITTER: IRM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
LENGTH: 249 amino acid
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Best Local Similarity
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-105-343A-2
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                                                                                                                      177 PDIQYPDATDEDITSHMESEELNGAYKAIPVAQDLNAPSDWDSRGKDSYETSQLDD-QSA 235
                                                                                                                                                                                                                               236 ETHSHKQSRLYKRKA---NDESN---EHSDVIDSQELSKVSRE----FHSHEFHS-HED 283
118 HQSDESHHSDESDELVTDFPTDLPATEVFTPVVPTVD-TYDGRGDSVVYGLRSKSKKFRR 176
                                                                 DSASSASNDDNVFDDFTSY 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------DSASSASNDDNVFDDFTSYNAH 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 DPSQKQNLLAPQTLPSKSNESHDHMDDMDEDDDDHVDSQDSIDSNDSDDVDDTDDSHQS 88
                                                                                                                                                                                    200 NAHKKKOERKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 VDDVGADYED--YTDMLNKL--NNAHTGTTPTSETTAEGEGET--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIF: 19103
ZIF: 19103
CONDUTER READMBLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/712,476A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5304496ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/07712476A
Patent No. 5304496
GENERAL INFORMATION:
APPLICANT: Hoyer et al.
TITLE OF INVENTION: Biological Regulation of
TITLE OF INVENTION: Mineralization
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                             LLV--RKARSEDSRPAAHFHLSSRRHQ 285
                                                                                                                                                                                                                                                                                                                                                     :|| |:: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Suzanne E. Miller
REGISTRATION UNDBER: 32,279
REFRENCE/DOCKET NUMBER: UPN
TELECOMMUNICATION INFORMATION:
TELEPAN: (215) 568 3100
TELEPAX: (215) 568 3439
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Suzanne E. Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 282 amino acids TYPE: AMINO ACID
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-07-712-476A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                        5 VICFCLLGITCAI---PVKQADSGSSEKQLYN------KYPDAVATWLNPD 47
                                                                                                                                                                                                                                                                                                             Query Match 5.4%; Score 116; DB 6; Length 300;
Best Local Similarity 23.1%; Pred. No. 0.0099;
Matches 75; Conservative 32; Mismatches 101; Indels 116; Gaps
                                                RESULT 15
5340934-6
; PACENT NO. 5340934
; ROBEY, PAMELA G.
; TITLE OF INVENTION: CDNA SEQUENCES OF HUMAN BONE MATRIX PROTEINS
; UNRERN APPLICATION: US/07/432,044
; FILING DATE: 03-NOV-1989
; SEQ ID NO: 6:
LENGTH: 300
212 VSGLLALRPGSSLRIRTL---PWAHLKAAPFLTYFGLFQV 248
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Search completed: September 13, 2004, 10:36:16 Job time : 20 secs

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(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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September 13, 2004, 10:35:34 ; Search time 131 Seconds OM protein - protein search, using sw model Run on:

(without alignments) 1001.237 Million cell updates/sec

US-09-813-329-6 2162 1 WTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1335176 seqs, 320689617 residues Searched:

fotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:*

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18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 6, Appli Sequence 2, Appli Sequence 54, Appli Sequence 64, Appl Sequence 64, Appl Sequence 148.75, Sequence 154595, Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 3, Appli Sequence 3, Appli Description US-09-813-329-6
US-09-813-329-4
US-09-813-329-2
US-09-813-329-54
US-09-813-329-64
US-10-437-963-148275
US-10-437-963-148275
US-10-437-963-154595
US-10-408-765A-434
US-10-408-765A-434 US-10-116-016-34 US-10-103-313-555 US-10-222-020-34 US-09-813-329-8 SUMMARIES Query Match Length DB Score Result

US-09-729-658B-2

Sequence 42, Appl Sequence 42, Appl Sequence 6, Appli Sequence 46, Appli Sequence 6, Appli	Sequence 250021, Sequence 137252, Sequence 18876, Sequence 28, Appl	Sequence 12955, Ap Sequence 12955, A Sequence 7025, Ap Sequence 7025, Ap	1 1 9 8 4 8 8 7 1 1 1 9 8 4 8 9 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	6 1 3 3 6 4 6 6	Sequence 1, Appli Sequence 227, App Sequence 172, App Sequence 303, App Sequence 336, App
US-10-202 US-10-218 US-10-012 US-10-310 US-10-719	US-10-424-599-250021 US-10-437-963-137252 US-10-424-599-188876 US-0479-435-28		US-10-437-1963 US-10-0382-182 US-10-032-583 US-10-437-963 US-10-467-243	US-10-171-311-176 US-10-205-823-307 US-10-177-293-340 US-10-301-822-147 US-10-303-55-6	
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16 17 19 20	22222	22 2 2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	, w w w w w	2 W W W 4 4	4 4 4 4 1 5 6 4 6

ALIGNMENTS

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Sequence 6, Application US/09813329

Batent No. US20020012968A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Variants Thereof
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 6/190,816
PRIOR APPLICATION NUMBER: 6/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
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100.0%; Score 2162; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 4.1e-167;
Matches 409; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Drosophila melanogastor US-09-813-329-6
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US-09-813-329-6
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Suibb Company
APPLICANT: Bristol-Myers Suibb Company
TITLE OF INVENTION: No. US20020012968Alel Drosophila Tumor Necrosis Factor Class MolecTITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Version 3.0
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Batent No. US20020012968A1

Belent No. US20020012968A1

GENERAL INFORMATION:

APPLICANT: Bristcol-Myers Suibb Company

TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Molec

TITLE OF INVENTION: Variants Thereof

FILE REFERENCE: D0016, np

CURRENT APPLICATION NUMBER: US/09/813,329

CURRENT APPLICATION NUMBER: 60/190,816

PRIOR APPLICATION NUMBER: 60/190,816

PRIOR APPLICATION NUMBER: 60/190,816

PRIOR APPLICATION NUMBER: 60/190,816

PRIOR APPLICATION NUMBER: 5000-03-21

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin version 3.0

SEQ ID NO 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 KESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERNSYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCLNTVPTN
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                                                                                                                                                                                                                                                                                                                                         Length 409;
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 96.3%; Pred. No. 1.3e-157;
Matches 394; Conservative 2; Mismarches 10
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                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Drosophila melanogastor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-54
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GENERAL INCORNATION:
GENERAL INCORNATION:
APPLICANT: Bristol-Myers Suibb Company
TITLE OF INVENTION: No. US20020012968Alel Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT APPLICATION NUMBER: 60/190,816
PRIOR APPLICATION NUMBER: 60/190,816
NUMBER: OF SEQ ID NOS: 65
SOFTWARE: Patentin Version 3.0
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 YIGNDNERNSYQGHFQTRDGVLTVTNTGLXYVYAQICYNNSHDQNGFIVFQGDTPFLQCL 354
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241 KESPAPLHHRRRWHSRHRHLLVRKARSEDSRPAAHFHLSSRRHQGSMGYHGDMYIGNDN
                                                                                                                              ERNSYQCHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQCDTPFLQCLNTVPTN
                                                                                                                                                      KESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEATS
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                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09813329
Patent No. US20020012968A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Drosophila melanogastor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09813329
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US-09-813-329-4
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APPLICANT: EMERHARDY, INES
APPLICANT: EMERHARDY, INES
APPLICANT: EMERHARDY, INES
APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEKWANS, RIERA JOSEPHINA
ITILE OF INVENTION: BAST AND FUNGI
FILE REFERENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
CURRENT FILING DATE: 2003-06-19
PRIOR PILING DATE: 2001-01-04
PRIOR PLILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFTWARE: Petentin version 3.1
SEQ ID NO 448
                                                                                                                                                                                                                             : :| : ::: ||: ::: | 273 KSKRRGRSSRRKKRSNDTASEGSSEEAVAAASGSSPSPLRDSKKKSRSSRRKRSKQSD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 SDDEEDKEDKEAEKUNKDSEDSENEKVEEDNKDTSSDSSSSSDSKSDSSSSSDSSSS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::| |: | : | |: | 306 PEDKKRKHTDDIKEEKPVKKFKNESESSASSSTDSIPATPEPELKPGQRKHFSRIDRSKV 365
                                                                                                      168 PTSET-----TAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNE 219
                                                                                                                                 220 EQNIQGNHTELQEKSSNE------ATSKESPAPLHHRRRMHSRHRHLLVRKAR 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 FDDFTSYNAHKKKQERKSRSIADVRNE---EQNIQGNHTEL---QEKSSNEATSKESPAP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 NFENSVLQDNTYKGAAGTWGEKASEKLLQVRGKDFTKNKNKMKRGSYKG-----GSITL 419
            108 PKKVDGLTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTT 167
                                         82 QQR----LGINYLDEFDEFQKEYENALIDYPKK---VDGLTDEEDDDDGDGLDSIADDED 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 DDVSYSSVD-DVGADYEDYTDMLN-KLNNAHTGTTPTSETTAEGEGETDSASSASNDDNV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 LHHRRRMHSR--HRHLLVRKARSE-----DSRPAA-------HFHLSSRRR- 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 ------HQGSMGYHGDM----YIGNDN--ERNSYQGHFQTRDGVLTV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 QLIPLV-LGFIGLGLVVAILALTIWQTTRVSHLDKEL-------KSLKRVVDNL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 141; DB 16; Length 428;
; Pred. No. 0.0063;
68; Mismatches 138; Indele 84; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 448, Application US/10451467A; Publication No. US20040161840A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CONTRERAS, ROLAND HENRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 20.8%;
Matches 76; Conservative 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                          267 SEDSRPA 273
                                                                                                                                                                                                                                                                                                                                        333 SEDQAPS 339
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                                                                                                                                                                                                                           Sequence 64, Application US/09813329

Patent No. US20020012968A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Suibb Company

TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole

TITLE OF INVENTION: Variants Thereof

FILE REFERENCE: D0016.np

CURRENT APPLICATION VMBER: US/09/813,329

CURRENT APPLICATION NUMBER: 60/190,816

PRIOR APPLICATION NUMBER: 60/190,816

PRIOR FILING DATE: 2000-03-21

NUMBER OF SEQ ID NOS: 65

SOFTWARE: Patentin version 3.0

SEQ ID NO 64
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 148275
LENGTH: 511
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23.5%; Pred. No. 0.0035;
tive 49; Mismatches 85; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 27;
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US-10-437-963-148275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.9%; Score 149; DB 9; L
Local Similarity 100.0%; Pred. No. 3.5e-05;
He 27; Conservative 0; Mismatches 0;
         Pred. No. 3.5e-05;
100.0%; Prec. ...
                                                                           311 TRDGVLTVTNTGLYYVYAQICYNNSHD 337
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bukharov, Andrey A.
                                                                                                      1 TRDGVLTVTNTGLYYVYAQICYNNSHD 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-64
         Best Local Similarity 100.
Matches 27; Conservative
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ORGANISM: Oryza sativa
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US-09-813-329-64
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                                                                                                                                             253 DDDDDDDDVSIEYRHQA------HRHQGHGIEEDEDVSDGHHHRDPSHRHRSHEEDDN 305
                                                                                                                                                                                                                                                                                    192 VFDDFTSYNAHK--KKOERKSRSIADVRNE-----EQNIQGNHTELQEKSSNEATSKES 243
                                                                                                                                                                                                      DVSYSSVDDVGADYEDYTDMLNKLNNAHTG-TTPTSETTAEGEGETDSA---SSASNDDN 191
                                                                                                                                                                                                                                                                                                                    -----RRRMHSRHRHLLVRK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
LOCATION: (179)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                  366 POHVHHGLVDEEEEEEITVQFGHYVASHQPRGHKSDEEDFQDEYKTEVPHHHHRVPRE 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 KRVVD-----NLQQRLG-----INYLD-----EFDEFQKEYENALIDYPKKVDG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 ---LTDEEDDDGGGGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 ETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTEL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 QEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARS-----EDSRPAAHFHLSSRRRHQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 FPAKATSTATAQRRTRQLIPLVLGFIGLGLVVA----ILALTIWQTTRVSHLDKELKSL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 FARRISCNRCGREKTIEAKMMKAGGIEIGKTLAEKSRGLFSANDWOCKTCSNVNWARRSE 94
                                                                                                                       ---GLDSIADDEDD
                                                                            Gaps
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                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426 EDERVSAELGHQAPSHRQSHQDEFTGHGQR--GSIKEMSHHPPGHTVVKD 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 ARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNERNSY-QGHFQTRD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96;
                                 Length 699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Application US/09764848
Patent No. US20020077270A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ08
CURRENT APPLICATION NUMBER: US/09/764,848
CURRENT FILING DATE: 2001-01-77
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.2%; Score 135; DB 9; Length 330;
21.2%; Pred. No. 0.014;
Live 48; Mismatches 108; Indels
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ----EDEDEDDADLSKYN----LDASEEEDSNKKKSNRRSRS----
                             Query Match
6.3%; Score 137; DB 16;
Best Local Similarity 20.7%; Pred. No. 0.026;
Matches 60; Conservative 38; Mismatches 116;
                                                                                                                  91 DEFDEFQKEYENALIDYPKKVD---GLTDEEDDDDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                            244 PAPLHH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-764-848-34
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Best Local S:
Matches 68,
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                                                                                 RESULT 8
US-10-437-963-154595
US-10-437-963-154595
Sequence 154595, Application US/10437963
Sequence 154595, Application US/10437963
Sequence 154595, Application US/10437963
Sequence 154595, Application No. US20040123343A1
Septicant: La Rosa, Thomas J.
APPLICANT: Expon, Yinha
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 30-216322)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 154595
LENTH: 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 LIDYPKKVDGL-----TDEEDDDDGDGL--DSIADDEDDDVSYSSVDDVG-ADYEDYT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::||:
287 EVLNQ------EGGDNNSDGDGEIEPVTDDDDIDDVGQQWCPTWEHRKFEQ----- 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DMINKLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fand, Bing
APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660088.465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 434
LENGTH: 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT4530_5443C.1.pep
US-10-437-963-154595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 434, Application US/10408765A; Publication No. US20040101874A1; GENERAL INFORMATION: APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Boin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-434
319 TNTGLY 324
                                      420 A-SGSY 424
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US-10-408-765A-434
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ORGANISM: Homo sapiens
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NAME/KEY: misc feature
LOCATION: (179)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 ---LIDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 ETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTEL 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : : : | | : : | | : | 35 FARTSCNRCGREKTTEAKMMARAGGTEIGKTLAEKSRGLFSANDWQCKTCSNVNWARRSE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          96;
                                                                                           Sequence 34, Application US/10116016; Publication No. US20030054379A1; GENERAL INPORMATION:
; FENERRAL INPORMATION:
; TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies; CURRENT APPLICATION NUMBER: US/10/116,016; CURRENT FILING DATE: 2002-04-05; Prior Application removed - See File Wrapper or Palm; NUMBER OF SEQ ID NOS: 53; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.2%; Score 135; DB 14; Length 330; 21.2%; Pred. No. 0.014;
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                   275 GSSSPRKRSYSSSSSSPERN 294
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68; Conservative
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ORGANISM: Homo sapiens
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US-10-116-016-34
                                                                       RESULT 11
US-10-116-016-34
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114 ---LTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTS 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARS-----EDSRPAAHFHLSSRRHQ 285
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                                                                                                                                                                                                                                                                                                                         20 FPAKATSTATAQRRTRQLIPLVLGFIGLGLVVA----ILALTIWQTTRVSHLDKELKSL 74
                                                                                                                                                                                                                                                                                                                                                             | :: | : | | : : | : | 35 FARRTSCNRCGREKTTEAKMMKAGGTEIGKTLAEKSRGLFSANDWQCKTCSNVNWARRSE
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TILLE OF INVENTION:
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TILLE REFERENCE: P7208C2
CURRENT APPLICATION UNMBER: US/10/222,020
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 10/116,016
PRIOR PLING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/764,848
PRIOR APPLICATION NUMBER: 09/764,848
PRIOR APPLICATION NUMBER: 60/119,065
PRIOR PELING DATE: 2000-01-17
PRIOR PELING DATE: 2000-02-04
PRIOR PLING DATE: 2000-02-04
PRIOR PLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR PELING DATE: 2000-06-28
PRIOR PELING DATE: 2000-06-28
PRIOR PLING DATE: 2000-06-38
PRIOR PLING DATE: 2000-06-34
PRIOR PLING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR PLING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR PLING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR PLING DATE: 2000-07-21
                                                                                                                                                                                        6.2%; Score 135; DB 14; Length 330; 21.2%; Pred. No. 0.014;
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                                                                                                                                                                                                                                                          48; Mismatches 108;
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APPLICATION NUMBER: 60/226,868
FILING DATE: 2000-08-22
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Publication No. US20030175739A1
GENERAL INFORMATION:
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FEATURE:
NAME/KEY: misc feature
LOCATION: (179)
OTHER INFERMATION: Xaa
US-10-103-313-555
                                                                                                                                                                                                                            Similarity
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PRIOR FILING DATE: 2000-07-07
PRIOR PRIOR PLING DATE: 2000-06-14
PRIOR PRIOR PLING DATE: 2000-06-14
PRIOR PRICATION WINBER: 60/216, 880
PRIOR PRICATION WINBER: 60/215, 270
PRIOR PLING DATE: 2000-06-14
PRIOR PLING DATE: 2000-06-14
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PRIOR FILING DATE: 2000-10-13
PRIOR PRICATION NUMBER: 60/239, 935
PRIOR PAPLICATION NUMBER: 60/239, 935
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-11-08
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PRIOR PILING DATE: 2000-09-09
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PRIOR PILING DATE: 200

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APPLICANT: Zonana et al.
TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
FILE REFERENCE: 55924
CURRENT APPLICATION NUMBER: US/09/729,658B
CURRENT FILING DATE: 2000-12-04
FRIOR APPLICATION NUMBER: 09/342,681
FRIOR FILING DATE: 1999-06-29
FRIOR PILING DATE: 1998-07-09
FRIOR APPLICATION NUMBER: 60/12,366
FRIOR APPLICATION NUMBER: 60/112,366
FRIOR APPLICATION NUMBER: 60/112,366
FRIOR PILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 1.22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 391
                                                                                                                                                                                              264 KARSEDSRPAAHFHLSSRRRHQGS-MGYHGDMYIG--NDNER---NSYQGHFQTRDGVLT 317
                                            264 KARSEDSRPAAHFHLSSRRHQGS-MGYHGDMYIG--NDNER---NSYQGHFQTRDGVLT 317
                                                                                                                                                     318 VINIGLYYVYAQ -- ICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIH 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 VINTGLYYVYAQ -- ICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIH 375
                                                                            240 KAGTRENQPAV-VHLQG----QGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 VLVDGTYFIYSQVEVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTN-YNTCYTAGVCL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Gaps
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Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                     |: ::| :| :| : ::| | 354 LKARQKIAVKMVHADIS--INMSKHTTFFGAIRL 385
                                                                                                                                                                                                                                                                  376 LERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376 LERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.1%; Score 132; DB Best Local Similarity 28.6%; Pred. No. 0.03; Matches 44; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: September 13, 2004, 10:46:53 Job time : 133 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09729658B Publication No. US20030023991A1 GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Suibb Company
ITILE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
ITILE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION UNMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR APPLICATION NUMBER: 60/190,816
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 CNMCNTPKYAKLEERTGYGGFNERENVEYIEREESDGEYDEFGRKKKK----YRGKAVG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 ---LTDEEDDDDGDGLDSIADDEDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTEL 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 KSRSSHSRSSSRSSSSRSRSRSRSSSSSSSSSSSSSRSRERSRSRSSKSRSSSRSHR 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 FPAKATSTATAQRRTRQLIPLVLGFIGLGLVVA----ILALTIWQTTRVSHLDKELKSL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : : | | : : | | : : | 35 FARRISCNRCGREKTTEAKMMKAGGTEIGKTLAEKSRGLFSANDWQCKTCSNVNWARRSE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 6.2%; Score 135; DB 14; Length 330; 1 Similarity 21.2%; Pred. No. 0.014; 68; Conservative 48; Mismatches 108; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 6.1%; Score 132; DB 9; Length 391; al Similarity 28.6%; Pred. No. 0.03; 44; Conservative 31; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/233,063
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,397
PRIOR FILING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,399
PRIOR PELING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence B, Application US/09813329
; Patent No. US20020012968A1
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ORGANISM: Drosophila melanogaster
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Matches 68; Conserval
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Matches 44; Conserva
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US-09-813-329-8
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 13, 2004, 10:32:13; Search time 19 Seconds (without alignments) 2070.649 Million cell updates/sec Run on:

US-09-813-329-6 2162 1 MTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV 409 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* **Database** :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	υ	hypothetical prote		chromodomain helic	glutamate synthase	histidine rich cal	homeotic protein c	probable transcrip	hypothetical prote			ų	IFH1 protein - yea	probable peptide-a	hypothetical prote	zinc finger protei	MAK16 homolog PFB0	F8K7.2 protein - A	hypothetical prote	DNA-directed RNA p	asparagine/asparta	hypothetical prote		polyprotein - Arab	_	U	hypothetical prote	
SUMMARIES	ID	869625	A34373	S64951	A71623	T13944	T28635	A54660	803170	T18233	S19365	G71609	T21259	T03377	855352	T18861	A89959	T41390	G71621	A86349	T46237	T28156	T18402	T10215	H96770	T31353	H84590	744		S64603
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æ	Query Match	7.7	7.1	6.7	6.4	6.4	6.4	6.3	6.3	6.2	6.2	6.2	6.0	6.0	6.0	ω. 9		•		•	٠	•	•	5.7	5.7	5.7	5.7		5.7	5.7
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osteopontin precur	hypothetical prote	hypothetical prote	myoD protein inhib	gene suppressor-of	hypothetical prote	osteopontin precur	hypothetical prote	osteopontin precur	protein P120 - Myc	hypothetical prote	hypothetical prote	hypothetical prote	Ap-3 adaptor compl	protein kinase agg	hypothetical prote
809575	G86311	T30321	T03744	806028	B96695	A37818	B89921	GEPGO	T18352	B71609	H84463	T29776	T18295	S35423	G86155
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314	669	292	675	964	5138	294	6713	303	1078	665	770	1046	1105	1067	290
5.6	5.6	9.6	9.6	9.9	9.6	5.6	9.6	5. 5.	5.5	5.5	5.5	5.5	5,5	5.5	5.4
ณ	21.5	121	120.5	120.5	120.5	120	120	119.5	119.5	119	119	118.5	118.5	118	117.5
121.	7														

ALIGNMENTS

RESULT S69625 Dypoth C; Date C; Date R; Date A; Refe A; Refe A; Refe A; Gene A; Gene A; Gene A; Gene	RESULT 1 S69625 hypothetical protein YDR457w - yeast (Saccharomyces of Species: Saccharomyces cerevisiae C;Decies: Saccharomyces cerevisiae C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #t C;Accession: S69625 R;Dietrich, Fs. R;Dietrich, Fs. R;Dietrich, Fs. R;Dietrich, Fs. R;Dietrich of the sequence of S. cerevisiae cosmids A;Description: The sequence of S. cerevisiae cosmids A;Reference number: S69554 A;Accession: S69625 A;Accession: S69625 A;Accession: S69625 A;Accession: S69625 A;Accession: S69625 A;Genetics:	RESULT 1 S69625 Nypothetical protein YDR457w - yeast (Saccharomyces cerevisiae) C.Species: Saccharomyces cerevisiae C.Species: 22-Aug-1996 #sequence_revisiae C.Species: 22-Aug-1996 #sequence_revisiae C.Species: 22-Aug-1996 #sequence_revisiae C.Species: 22-Aug-1996 #sequence_revisiae C.Species: 22-Aug-1996 #sequence_revisiae C.Species: 23-Aug-1996 #sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996 #sequence of S. Cerevisiae Cosmids 9410, 8035, 8166, and 9787. A.Species: 23-Aug-1996, 8166, and 9787. A.Species: 23-Aug-1996, 8166, and 9787. A.Species: 23-Aug-1996, 8166, and 9787. A.Species: 23-Aug-1996, 8166, and 9787. A.Species: 2
Que: Best Mato	7.7%; Score 165.5; DB 2; Ouery Match Best Local Similarity 19.4%; Pred. No. 0.028; Matches 78; Conservative 66; Mismatches 142;	Score 165.5; DB 2; Length 3268; Pred. No. 0.028; 5; Mismatches 142; Indels 117; Gaps 16;
λ _o q	51 VAILALTIWQTTRVSHLDKE : 1856 VAVEALNTISSTR	VAILALTIWQTTRVSHLDKELKSLKRVVDNLQQRLGINYLDBFDBFQKEYE 101 :
\chi_{\text{q}}	102 NALIDYPKKVDGLTDE :: 1901 NSALGMYDVEDIE	NALIDYPKKVDGLTDEEDDDDGDGLDSIADDEDDDVSYSS 141 :: NSALGMYDVEDIEEDDDDTSLIGDDDAMAFVDSDNGFEVVFSDEDDMGEED 1953
ò q	142 VDDVGADYEDYTDMLNKLNN : :: :: :: :: :: 1954 ADDARSDSEE-NELSSEMOS	VDDVGADYEDYTDMLNKLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTS 198 ADDARSDSEE-NELSSEMQSSTADGTDVDYEVDDADGLIINIDQPSGDDEEMADYDANIS 2012
oy op	199 YNAHKKKGERKSRSIADVRN ::: :: :: :: :: :: :: ::	YNAHKKKGERKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKES 243 :::
oy Op	244 PAPLHHRRRMHSRHRHLLVR :: 2072 DEPINSTRMGDSRRRWLIAE	PAPLHHRRRWHSRHKHLLVRKAR-SEDSRPAAHFHLSSRRHQGSMGYHGDMYLGNDNER 302 :
& g	303 NSYQCHFQTRDGVLTVTNTG : : : 2107 DRGVFRGIEHIFSNENEP	303 NSYQGHFQTRDGVLTVTNTGLXYVYAQICYNNSHDQNGFIVFQGDTPFLQCLNTVPTN 360 : : :
S G	361 MPHKVHTCHTSGLIHLE 2165 QSNLINPLGPTGLEQVENDI	361 MPHKVHTCHTSGLIHLERNERIHLKDI 387 : : : : : : 2165 QSNLINPLGPTGLEQVENDISDQVTVAGSGSRFRSHHLHFSEV 2207

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probable secreted protein PFB0115w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: N. 3. 21620
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Spertea, M.; Salzberg, S; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.,
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71620; MUID:99021743; PMID:9804551
A;Accession: A71623
A;Accession: A71623
A;Accession: A71623
A;Accession: BNA
A;Residues: 1-1192 cGAR>
A;Residues: 1-1192 cGAR>
A;Cross-references: GB:AE001373; GB:AE001362; NID:93845097; PIDN:AAC71813.1; PID:93845095
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Dec-2002
C;Accession: T13944
R;Stokes, D.G.; Tartof, K.D.; Perry, R.P.
Proc. Natl. Acad. Sci. U.S.A. 93, 7137-7142, 1996
A;Title: CHD1 is concentrated in interbands and puffed regions of Drosophila polytene chn A;Reference number: Z17823; MUID:96293489; PMID:8692958
                                                                                                                                                                                                QKEYENALIDYPKKVDGLTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDML 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           723 KEDNKEKDKEDD-----KEKHDKHVRRIKKKMKDDDYDES----LKTKNYYPHNMTFGQ 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 DMYIG--NDNERNSYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQ---- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRHQGSMGYHG 292
                                       157 NKLNNAHTGTTPTSETTAEGEGETDSASSASND-DNVFDDFTSYNA-HKKKQERKSRSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 GDTPFLQCLNTVP----TNMPHKVHTCHT-----SGLIHLERNERIHLKDIHND 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGIPKEQPYNNVPYILKKGLEPKTHN-HVKEDQPNIKQGVV---KGQEPHVDDMHNN 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                625 BIDLDDQEEDGEEDKEDDKEDDKEDDKEXDKED------DXEKYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 EGEGETDSASSASND--DNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      773 QQYFPYXNPLEQQNYQLHH------IIKQQQNYHPHHIIKQQQNHNPHHLLQEQEKHHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 DKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYENAL----IDYPKKVDGLTDEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 ----DDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.4%; Score 138.5; DB 2;
Best Local Similarity 20.4%; Pred. No. 0.44;
Matches 73; Conservative 60; Mismatches 145;
                                                                                                                                                                                                                                                                                                  DVRNEEQNIQGNHTELQEKSSNEATSK 241
                                                                                                                                                                                                                                                                                                                                                     : | | : : | | : : | | ENFNEDETVADKDIEGGPESNKNSDSK 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: PFB0115w
                                                                                                                                                                                                                                                                                                  215
                                                                                                                                                                                                                                                                                                                                                                             694
                                                                                                                                                                                                                        647
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       A44373

histidine-rich calcium-binding protein precursor - rabbit

bistidine-rich calcium-binding protein precursor - rabbit

c;Species: Orycolagus cuniculus (domestic rabbit)

c;Date: O8-Uun-1990 #sequence_revision O8-Uun-1990 #text_change O5-Nov-1999

C;Accession: A44373

K;Hofmann, S.L.; Goldstein, J.L.; Orth, K.; Moomaw, C.R.; Slaughter, C.A.; Brown, M.S.

J. Biol. Chem. 264, 18083-18090, 1989

A;Title: Molecular cloning of a histidine-rich Ca(2+)-binding protein of sarcoplasmic reparcession: A4373; MUD:90036884; PMID:2808365

A;Reference number: A34373; MUD:90036884; PMID:2808365

A;Residues preliminary

A;Molecule type: mRNA

A;Residues: 1-852 cHOF>

A;Cross-references: GB:J05080; NID:g165099; PIDN:AAA31279.1; PID:g165100

C;Keywords: calcium binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nypothetical protein YLR114c - yeast (Saccharomyces cerevisiae)

hypothetical protein YLR114c - yeast (Saccharomyces cerevisiae)

hypothetical protein L2341

C; Adecesian: Saccharomyces cerevisiae

C; Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 19-Apr-2002

C; Accession: S64951, S69401

R; Verhasselt, P.; Voet, M.; Volckaert, G.

submitted to the Protein Sequence Database, May 1996

A; Reference number: S64943

A; Reference number: S64943

A; Residues: 1-764 <VER.

A; Residues: 1-764 <VER.

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A,Residues: 1-764 <VEW>
A,Cross-references: EMBL:X89514; NID:g1297019; PIDN:CAA61692.1; PID:e198747; PID:g129702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 DEEDDDDGDGLDS------IADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAH 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 DEDDDDEGDSTESDRHQAHRHRGHREEEDDDDD-----DDEG----DSTESDRHQAHRH 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 TGTTPTSETTAEGEGETDSA------SSASNDDNVFDDFTSYNAHKKKQERKSR 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :::: | | | | | | | 403 EBEDEDDDEGDSTESDHHQAHRHRGHREBEDEEDDDEGDSTESDRHQAHRHRGHGEEED 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 RGHREEEDEDDDDEGDSTESDRHQAHRHRGHREEEDEDDDBGDSTESDRHQAHRHRGHR 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 SIADVRNEEQ------NIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRH 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 LLVRKARSEDSRPAAHFHLSSRRRHQGSMGYH----GDMYIGNDNERNSYQGH 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.1%; Score 153.5; DB 2; Length 852; Best Local Similarity 22.7%; Pred. No. 0.033; Matches 53; Conservative 31; Mismatches 88; Indels 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 764;
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A;Cross-references: SGD:S0004104
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A;Accession: 869401
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T28635
glutemate synthase (NADH2) (EC 1.4.1.14) - malaria parasite (Plasmodium falciparum)
C;Species: Plaemodium falciparum
C;Species: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Jun-2002
C;Accession: T28635
R;Cowan, G.M.
S;Reference number: 220490
A;Reference number: 220490
A;Reference number: 20490
A;Reference number: DNA
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-3097 cCOM>
A;Cross-references: EMBL:Y17045; NID:e1286063; PID:e1286064; PIDN:CAA76602.1
C;Genetics:
A;Genetics:
A;Genetics:
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 -----SYSSVDDVGADYEDYTDM-----LINKLNNAHTGTTPTSETTAEGEGETDS 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 KVDGLTDEEDDDDGDGLDSIADDEDDVSYSSVDDVGADYEDYTDMLNK-LNNAHTGTT- 167
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A;Status: preliminary; Lieunerical A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Cross-treferences: EMBL:L7907; NID:g1448982; PID:g1448983; PIDN:AAC37264.1 C;Genetics: A;Gene: CHD-1 A;Cross-references: FlyBase:FBgn0016132 A;Cross-references: FlyBase:FBgn0016132 C;Superfamily: chromodomain helicase CHD1; chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Keywords: DNA binding C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-family: Chromobox homology C;Cross-fami
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1 Similarity 23.7%; Pred. No. 1.4;
49; Conservative 33; Mismatches 70;
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Pred. No. 0.76;
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Best Local Similarity 24.5%;
Matches 52; Conservative 36
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Matches 49; Conserv
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RESULT 7 A54660 histidine rich calcium binding protein - human

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C;Species: Homo sapiens (man)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 05-Nov-1999
C;Dates: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 05-Nov-1999
C;Accession: A54660
R;Hofmann, S.L.; Topham, M.; Haieh, C.L.; Francke, U.
Genomics 9 656-669, 1991
A;Title: CNNA and genomic cloning of HRC, a human sarcoplasmic reticulum protein, and lo A;Reference number: A54660; MUID:91244309; PMID:2037293
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila
Silothinger, K.; Bodmer, R.; Jack, J.; Jan, L.Y.; Jan, Y.N.
Nature 333, 629-635, 1988
A;Title: Primary structure and expression of a product from cut, a locus involved in species on the structure and expression of a product from cut, a locus involved in species (S03170).
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C;Superfamily: homeotic protein cut; cut repeat homology; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
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A;Molecule type: mRNA
A;Residues: 1-699 <HOF>
A;Cross-references: GB:M60052; NID:g183918; PIDN:AAA88071.1; PID:g183919
C;Genetics:
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A;Residues: 1-2175 <BLO>
A;Cross-references: EMBL:X07985; NID:g7767; PIDN:CAA30794.1; PID:g7768
C;Genetics:
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A,Cross-references: GDB:126369;
A,AMAp position: 19q13.3-19q13.3
C,Keywords: calcium binding
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RESULT 10 S190thefical C1Species: Sa C2,Date: 31.Ma C3,Date: 31.Ma C3,Date: 31.Ma C4,Date: 34.Ma C4,Date: 34.Ma C5,Date: 34.Ma C6,Date: 34.Ma C7,Date: 34.Ma C7,Coss-refer C6,Genetics: A6,Gene	Ouery Matches 5: Matches 5: Qy 137 Qy 186 Qy 186 Qy 238 Qy 238 Qy 290 Qy 290 Qy 290	Db 242 Qy 345 Db 281	RESULT 11 G7450theitcal proportion of Species: Place; Place; Place; Place; Place; Place; Place; Place; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea, M.; Pertea; Place
Db 227 PAATVATGAAAAAAATPIATGNVKSGSTTSNANHTNSNNSHQDEE	PESULT 9 T18233 probable transcription regulator protein - yeast (Candida albicans) C;Species: Candida albicans C;Date: 12-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T18233 R;Barrell, B.G.; Rajandream, M.A. R;Barrell, B.G.; Rajandream, M.A. R;Barrell, B.G.; Rajandream, M.A. A;Reference number: Z18831 A;Accession: T182333 A;Accession: T182333 A;Accession: T182333 A;Accession: T182333 A;Acc	Query Match Best Local S Matches 86	Db 146 LEGELDSLSGQSKRKGGSSIQSSIDDYKKIERNNSHISKLERVLENLDSPLD-PARID 204 Qy 113 GLTDBEDDDDGDGL

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.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, B.V.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; 1126-1132, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ype: DNA |
1-2500 «GAR»
rences: GB:AE001408; GB:AE001362; NID:g3845238; PIDN:AAC71919.1; PID:g384524(
al source: clone 3D7
                                                                                                                                                                                                                                                                                                                            rences: EMBL:X59720; NID:g1907116; PIDN:CAA42379.1; PID:g5326; MIPS:YCL037c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 omosome 2 sequence of the human malaria parasite Plasmodium falciparum.
number: A71600; MUID:99021743; PMID:9804551
G71609
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Similarity 21.1%; Pred. No. 2.4;
69; Conservative 44; Mismatches 124; Indels 90; Gaps 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 VSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSET------TAEGEGETDSASS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VSTISIEDL------DATRKKKM'--RTPTPKSSTATKWVPIKASITVSGTKRSGSKNG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 ASNDDN------VFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 ATSQENGQSTQQQQPPHHRNHHSHH------HNSNGPQRRKFHNSNNAGMPQNQGFP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 ATSKES-----PAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMG-- 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 ----YHGDMYIGNDNERNSYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVF 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DDEDDDVSYSSVDDVGADY--EDYTDML------NKLNNAHT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 GTTPTSET-TAEG---EGETD-------SASSASNDDNVFDDFTSYNAHK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eliminary; nucleic acid sequence not shown; translation not shown
| protein YCL037c - yeast (Saccharomyces cerevisiae)
Saccharomyces cerevisiae
(ar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000
$19365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein PFB0650w - malaria parasite (Plasmodium falciparum)
lasmodium falciparum
ov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 6.2%; Score 134; DB 2; Length 466; Similarity 21.4%; Pred. No. 0.28; 55; Conservative 32; Mismatches 92; Indels 7
                                                                                                                                             1.; Esteban, M.; Navas, L.
o the Protein Sequence Database, March 1992
number: S19365
                                                                                                                                                                                                                                                                                                                                                                                                               rences: SGD:S0000542; MIPS:YCL037c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QQQFYPVQPVLMAINNI 297
                                                                                                                                                                                                                                      : S19365
type: DNA
1-466 <DEL>
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ZmHox1b causes pleiot

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Note that the state of the maize homeobox genes ZmHoxla or ZmHoxlb can A; Reference number: Z14909; MUID:96361874; PMID:8721746
A; Reference number: Z14909; MUID:96361874; PMID:8721746
A; Reference number: Z14909; MUID:96361874; PMID:8721746
A; Reference number: Z14909; MUID:96361874; PMID:8721746
A; Reference number: Z14909; MUID:96361874; PMID:97463156.1; PID:91648931
A; Residues: 1-692 cUEB>
A; Residues: 1-692 cUEB>
A; Cross-references: EMBL:X92428; NID:91648930; PIDN:CAA63156.1; PID:91648931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aypothetical protein F22D6.5 - Caenorhabditis elegans
C.Species: Gaenorhabditis elegans
C.Species: Gaenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Toot-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T21259
R.Wilkinson, J.
submitted to the EMBL Data Library, April 1996
A.Reference number: Z13397
A.Reference number: Z13397
A.References realinary; translated from GB/EMBL/DDBJ
A.Residues: 1-775 < WIL>
A.Residues: 1-775 < WIL>
A.Residues: 1-775 < WIL>
A.Residues: 1-775 < WIL>
A.Residues: CESP:F22D6.5
A.Reperimental source: clone F22D6
C.Genetics:
A.Genetics: A.Genetics: A.Map position: 1
A.Introns: 43/1; 257/3; 303/3; 444/1; 628/1; 709/3; 739/3
                                                                             1021 SEEYTSEEYTSEGYTNEGYTNEQYINGQYINGQSIEDQSINDQSIED
                                                                                                                                                                                                                                                                                            ----- 1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 SSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 DSEDD-----EDD-----RKLAEAKDLIKSTRFGSEQGSGASTPVSIQSDNDTPTDFFSGL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 N---AHKKKQERKSRSIADVRNEEQNIQGN------HTELQEKSSNEATSKESPAPL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 RDKMVHMKD------ADEHNVDEVLQRGKDEEYREDWHTQLKEQEKREEEEK----- 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381 --KKKLEAEAAAEAAKKKKQEEDDTGFDMFADNEELPQDSTTIDGHSGAVHDTLKDNWDD 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 YQGHFQTRDG-----VLTVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCLNT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
T03377
Homeotic protein HOX1B - maize
C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                               204 KKQERKSRSIADVRNEEQNIQG---NHTELQEKSSNEATSKESPAPLHHRRRMHSRHRL
                                                                                                                                            LVRKARSEDSRPAA--HFHLSSRRRHQGSMGYH--GDMYIGNDNERNSYQGHFQTRDGVL
                                                                                                                                                                                                                                         TVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTFFLQCLNTVPTNMPHKVHTCHTSGLIHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 775;
                                                                                                                                                                                                                                                                                       1191 SSENPNVDDLSGHI----QNNDNSFNSSSSNVP----LNVNPTNI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.0%; Score 130.5; DB 2; Length Best Local Similarity 21.8%; Pred. No. 0.86; Matches 74; Conservative 49; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 VEGYYRVRIGELLDTRYRVVGFTGAG---VFGNVCRCNDQTKG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 VPTNMPHKVHTCHTSGLIHLERNERIHLKDIHNDRNAVLR 396
                                                                                                                                                                                                                                                                                                                                                                                    -ENSNILPLSIEGTNSAHLNFG--RSY 1251
                                                                                                                                                                                                                                                                                                                                       377 ERNERIHLKDIHNDRNAVLREGNNRSY 403
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IPHI protein - yeast (Saccharomyces cerevisiae)

NyAlternate names: protein L8083.9; protein YR223c; RRP3 protein
C;Species: Saccharomyces cerevisiae
C;Date: 10-oct-1995 #sequence revision 03-Nov-1995 #text_change 21-Jul-2000
C;Accesion: S55352, 551446; 547477
R;Cherel, I.; Thuriaux, P.
Yeast II, 261-270, 1995
A;Title: The IFHI gene product interacts with a fork head protein in Saccharomyces cerev
A;Reference number: S55352, MUID:95304839; PMID:7785326
A;Accession: S55352
                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                91 DEFDEFOKEYENALIDYPKKVDGLTDEEDDDDGDGLDSIADDED----DD----VSYSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 HKKKQERKSRSIADVR----NEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H---DEVSSPPLPDVKVGDMEKNTAQSNTTSSADDPMETEIDQSVVLPVSRRRQAERLDY 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 KRLYDEAYGEASSDSSDEEEWSGKNTPIKSNEEGEVGSPAGKGSRVAHHNELTTONTKES 539
                                                                                                                                                                                                                                                                                                                                                                                                                           142 VDDVGADYEDYTDMLNKLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLLVRKARSEDSRPAAHFHLSS-----RRRHQGSMG-----YHGDMYIGNDNER 302
                                                                                                                                                                                                                                                                                                                            317 NDFDPNMPEEHVA----SKEEGSSEEEEDDDG-GSDS--DDSDFLTCSDDLEPLIDKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 VDDLGLSSEDSED-----DYDPAGPDSDKDVEKKSNSDESDFTSDSDDFCKEIKKSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL: 229488; NID: 9531491; PIDN: CAA82624.1; PID: 9531492
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A,Cross-references: EMBL:U19027; NID:g609363; PID:g609372; MIPS:YLR223c
A;Gene: Hox1b
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.0%; Score 129; DB 2; Length 1085; Best Local Similarity 19.9%; Pred. No. 1.6; Matches 73; Conservative 48; Mismatches 126; Indels 120;
                                                                                                                                      6.0%; Score 129; DB 2; Length 692;
22.9%; Pred. No. 0.93;
tive 37; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: The sequence of S. cerevisiae cosmid 8083. A; Reference number: S$1443. A; Accession: S$1446
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submitted to the EMBL Data Library, December 1994
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A;Map position: 12R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1085 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NSYQGHFQTRDGVLTVTNTGL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540 LHSLHGSVDEKHGDLTSNGSNI 561
                                                                                                                                                                       Best Local Similarity 22.98
Matches 60; Conservative
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                                                                                                                                             Query Match
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148 DÖSDÖBDEDEBTÜSEÜDENIDEVKALTAGRKRAMKALSAMWTNETLÄSERENKK 201 161 NAHTOTTPESETTRE
161 NAHTOTTPSETTAE. 202 NKSVKLSPKKENEEDGKEEKEKERGOKQGESNKKEVNGSGTTATGOALGFRFKKEDDG 261 202 NKSVKLSPKKENEEDGKEEKEKERGOKQGESNKKEVNGSGTTATGOALGFRFKKEDDG 261 197 TSY-NAHKKKOGREKSPLDLAGNEENGAGGESNKEVNGSGTTATGOALGFRFKKEDDG 261 262 ISFGNGNEGYNEDICEFLDLAGNEENGAGGESNKEVNGSGTTATGOALGFRFKKEDDG 261 262 ISFGNGNEGYNEDICEFLDLAGNEENGAGGESNKEVNGSGTTATGOALGFRFKKEDDG 293 264 SPELHHRRENGSRHHHLLVKKARSEDSRPAHFHLSSRRRHQGSNGYHODMYTGND 299 265 ISFGNGNEGYNEDICEFLDLAGNEENGARGENGARGHTLINEELRPPNISESDESE319 266 SADON NEENYDIDODAYPDINNEDSRGSGTDLETGEDDEIDILEE 356 300 NEENYONGGHFOTRDGYLIVVNTGLYTVYAG-ICTNNSHDGNGSPLYGG 345 317 EFGNIVSELCANDDELSFDGSIHEBGSDPYEDARKFLANGSRGSTGDLETGEDDEIDILEE 356 318 GGTPPLG 335 417 FDMFFYE 423 318 GGTPPLG 335 417 FDMFFYE 423 318 GGTPPLG 335 417 FDMFFYE 423 318 GGTPPLG 335 417 FDMFFYE 423 318 GGTPPLG 335 417 FDMFFYE 423 318 GGTPPLG 335 318 GGTPPLG 335 326 Cacession: T18861, T23533 326 Cacession: T18861, T23533 326 Cacession: T18861, T23533 326 Cacession: T18861, T23533 326 Cacession: T18861, T23533 327 EFGUNES ENEL.Z79556, NDD-61323798; PIDN:CAB01859.1; GSPDB:GN00028; CESP:K093, GASCGSSTGOALGOALGES ENEL.Z79563; NDD-61323798; PIDN:CAB01859.1; GSPDB:GN00028; CESP:K093, GASCGSSTGOALGOALGES ENEL.Z79563; NDD-61323798; PIDN:CAB01859.1; GSPDB:GN00028; CESP:K093, GASCGSSTGOALGOALGES ENEL.Z79563; NDD-61323798; PIDN:CAB01859.1; GSPDB:GN00028; CESP:K093, GASCGSSTGOALGOALGES ENEL.Z79563; NDD-61323798; PIDN:CAB01859.1; GSPDB:GN00028; CESP:K093, GASCGSSTGOALGOALGES ENEL.Z79561; PIDN:CAB01887.1; GSPDB:GN00028; CESP:K093, GASCGSSTGOALGOALGES ENEL.Z79561; PIDN:CAB01887.1; GSPDB:GN00028; CESP:K093, GASCGSSTGOALGOALGES ENGL.Z79561; PIDN:CAB01887.1; GSPDB:GN00028; CESP:K093, GASCGSSTGOALGOALGOALGES ENGL.Z79561; PIDN:CAB01887.1; GSPDB:GN00028; CESP:K093, GASCGSSTGOALGOALGOALGOALGES ENGL.Z79561; PIDN:CAB01887.1; GSPDB:GN00028; CESP:K093, GASCGSSTGOALGOALGOALGOALGOALGOALGOALGOALGOALGOAL
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197 TSY-NAHKKKORRKSRSIADVRNEEGNIQGNHTELGEKSSNEATSKESP 244 262 ISCALANDERNEEGNEEGNEEGNEEGNEEGNEEGNEEGNEEGNEEGNE
245 APLHHRRNGHSRHRHLVRKARSEDSRPAMIFHLSSRRHQGSNGYHODWIGND 299 320
320YDIDODAYEDVINEDSHGEIGTDLETGEDDIPLIEE 356 300 NERNYOUG-HEQTREDGYLTVTNTGIZTVTVAQ-1CTNNSHDONGFIVFO 345 15 TECNIVSELQNDDELSFDGSIHEEGSDPVEDAENKFLQNETNGENGYDEEDDEEDELMSD 416 340 GDTPFLQ 352 417 FDMFFYE 423 5ULT 15 5
300 NBENASYOGHPOTRDGVLTVTNTGLYVYAQ-ICYNNSHDOWGFIVPQ 345 357 EECNIVOSELGNDDELSPDGSIHEEGSDPVEDAENKELGNEYDEEDEEDEEIMED 416 346 GDTPPLQ 352 417 FDMFPYE 423 417 FDMFPYE 423 417 FDMFPYE 423 417 FDMFPYE 423 417 FDMFPYE 423 417 FDMFPYE 423 417 FDMFPYE 423 417 FDMFPYE 423 417 FDMFPYE 423 417 FDMFPYE 423 418 FDMPYE 423
357 EIGNTVSELQNUDELSFDGSIHEGGSDPVEDARNKFLQNEYNGENGYDEEDEEDEIMSD 416 346 GDTPFLQ 352 417 FDWRFYE 423 SBULT 15 417 FDWRFYE 423 SBULT 15 SBOLT 15 SBOLT 15 SBOLT 15 SBOLT 15 SPOCKES Canonynabolitis elegans Date: 15-Oct-1999 #text_change 18-Feb-2000 SACCESSION: T18661; T23533 BACCESSION: T18661; T23533 Date: 15-Oct-1999 #text_change 18-Feb-2000 SACCESSION: T18661 BACCESSION: T18661 BACCESSION: T18661 CRESTER TO THE MILE DATA LIDRARY, August 1996 Residues 1-872 SEALUS: Potliminary; translated from GB/EMBL/DDBJ MOLECULE type: DNA Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 Residues: 1-872 SEACH 1999 #text_change 1996 SEACH 1999 #text_change 1996 SEACH 1999 #text_change 1996 SEACH 1999 #text_change 1996 SEACH 1999 #text_change 1996 SEACH 1999 #text_change 1996 SEACH 1999 #text_change 1996 SEACH 1999 #text_change 1996 SEACH 1999 #text_change 1996 SEACH 1999 #text_change 1996 SEACH 1999 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990 #text_change 1996 SEACH 1990
346 GDTPPLQ 352 417 FDMPFYE 423 417 FDMPFYE 423 8861 Obable peptide-aspartate beta-dioxygenase (EC 1.14.11.16) - Caenorhabditis elegans obecies: Caenorhabditis elegans Species: Caenorhabditis elegans Date: 15-Oct-1999 #text_change 18-Feb-2000 Swinburne, J. Bantied to the EMBL Data Library, August 1996 Accession: TI8861, T23533 Accession: TI8861, T23533 Satus: preliminary; translated from GB/EMBL/DDBJ Reference number: 219032 Satus: preliminary; translated from GB/EMBL/DDBJ Reference mumber: 21973 Reference mumber: 21973 Reference mumber: 21973 Reference mumber: 21973 Accession: T2533 Reference mumber: 21973 Accession: T2534 Accession: T25354 Accession
SULT 15 Species: Caenorhabditis elegans Tobable peptide-aspartate beta-dioxygenase (BC 1.14.11.16) - Caenorhabditis elegans Tobable peptide-aspartate beta-dioxygenase (BC 1.14.11.16) - Caenorhabditis elegans Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 Accession: T18861; T23533 Swinburne, J. Bunitted to the EMBL Data Library, August 1996 Accession: T18861 Accession: T18861 Accession: T18861 Accession: T18861 Accession: T18861 Accession: T18861 Accession: T18861 Accession: T1886 Accession: T1886 Accession: T1886 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T2353 Accession: T33533 Accession: T33533 Accession: T
CONSERVATIVE 48; Mismatches 109; Indels 72; Gaps VYLDEFDEFOKEYENALIDYPKKVDGLTDRFDDDDGGLDGIDGIDGDDVVCVCVV
144 DVGADYEDYTDMLNKLANNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTS 198

Search completed: September 13, 2004, 10:35:52

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GenCore version 5.1.6
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                  Copyright
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- protein search, using sw model OM protein

September 13, 2004, 10:23:02; Search time 12 Seconds (without alignments) 1774.724 Million cell updates/sec Run on:

US-09-813-329-6 2162 1 MTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV 409 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

141681

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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YBE6_YEAST	EBA1_PLAFC YMJ3_YEAST	OSTK_BOVIN BCK2_YEAST	VTA2 XENLA OSTP BOVIN	GAT1_YEAST SG1 BOVIN	WRKG ARATH DSPP_HUMAN
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                   J. Blod. Chem. 264:18083-18090(1989).
-!- FUNCTION: May play a role in the regulation of calcium sequestration or release in the SR of skeletal and cardiac muscle.
-!- SUBCELLULAR LOCATION: Sarcoplasmic reticulum lumen.
                                                                                                                                                                                             TISSUE=Skeletal muscle;
MEDLINE=90036884; PubMed=2808365;
Hofmann S.L., Goldstein J.L., Orth K., Moomaw C.R., Slaughter C.A.,
Brown M.S.;
"Molecular cloning of a histidine-rich Ca2+-binding protein of
sarcoplasmic reticulum that contains highly conserved repeated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL. SARCOPLASMIC RETICULUM HISTIDINE-RICH
                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sarcoplasmic reticulum histidine-rich calcium-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPROXIMATE TANDEM REPEATS
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            852 AA.
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InterPro; IPR002134; HCP.
PROSITE; PS00328; HCP; 10.
Calcium-binding; Signal; Repeat.
SIGNAL 1 77 POJ
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            STANDARD;
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P16230;
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                                                                                                                                                                     DEEDDDDGDGLDS-----IADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAH 163
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                                                                                                                                                                                                                                                                      403 EEEDEDDDEGDSTESDHHQAHRHRGHREEDEEDDDEGDSTESDRHQAHRHKGHGEEED 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 9:656-669(1991).
-!- FUNCTION: May play a role in the regulation of calcium sequestration or release in the SR of skeletal and cardiac muscle.
-!- SUBCELLULAR LOCATION: Sarcoplasmic reticulum lumen.
-!- SIMILARITY: STRONG, TO RABBIT HRC.
                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                               Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Skeletal muscle;
MEDLINE=91244309; PubMed=2037293;
Hofmann S.L., Topham M., Hsieh C.-L., Francke U.;
"CDNA and genomic cloning of HRC, a human sarcoplasmic reticulum protein, and localization of the gene to human chromosome 19 and
                                                                                                                                    61;
 2-9.
2-9.
2-10.
4 X APPROXIMATE TANDEM REPEATS.
POLY-GLIV.
METAL-BINDING (POTENTIAL).
                                                                                                           DB 1; Length 852;
                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sarcoplasmic reticulum histidine-rich calcium-binding protein
                                                                                                                                  Indels
                                                                                    A43C0CB3E494B930 CRC64;
                                                                                          7.1%; Score 153.5; DB 1; 7%; Pred. No. 0.018;
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                                                                                   96117 MW;
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Matches 53; Conserv
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HRC OR HCP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 DDDDDDDDDVSIEYRHQA-----HRHQGHGIEEDEDVSDGHHHRDPSHRHRSHEEDDN
SARCOPLASMIC RETICULUM HISTIDINE-RICH CALCIUM-BINDING PROTEIN. GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88232956; PubMed=2897632; Blochlinger K., Bodmer R., Jack J., Jan L.Y., Jan Y.N.; Blochlinger K., Bodmer R., Jack J., Jan L.Y., Jan Y.N.; "Primary structure and expression of a product from cut, a locus involved in specifying sensory organ identity in Drosophila."; Nature 333:629-635[1988].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 ARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNERNSY-QGHFQTRD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                             1-4.
6 X APPROXIMATE TANDEM REPEATS.
2-2.
2-3.
                                                                                                                                                                                                                                                                                                                                 Length 699;
                                                                                                                                                                                                                                                                                                                              ; Score 137; DB 1; Length 69;
; Pred. No. 0.16;
38; Mismatches 116; Indels
                                                                                                                                                                                              2-5.
2-6.
METAL-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                     Missing. -
/FTId=VAR_011622.
: 9922EEDF012C61DD CRC64;
                                                         TANDEM REPEATS,
                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                        FTId=VAR_005623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HMCU DROME STANDARD; PRT; 2175 AA. P1015B0, O9W306; D01-WAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update) CT OR CGI1387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
                                                                                  \frac{1-2}{1-3}.
                                                                                                                                                                                                                                                                                                   80244 MW;
                                                                                                                                                                                                                                                                                                                                          Local Similarity 20.7
                         2004
33651
2213
2213
3365
1121
1121
1154
1154
673
673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 PAPLHH----
                                                                                                                                                                                                                                                                                                  699 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Berkeley;
                           193
246
106
106
134
106
134
1155
214
271
319
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m

GO:0008587; P:wing margin morphogenesis; NAS.

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RAM MEDLINEAZOUSHOOD, FURNEGAL-LOISILS, RAM AMBADINEAZOUSHOOD, PURNEGALS, MICKER RAM, HOSKING RAM, Galle R.F., R George R.A., Lewis S.E., Richards S., Abburner M., Henderson S.N., RA Gauton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Heiderson S.N., RA Bardon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikios G.L.G., Ballew R.M., Basu A., Baxendale J., Barktarogiu L., Besaley E.M., Ballew R.W., Basu A., Berman B.D., Bhandari D., Ballew R.W., Basu A., Berman B.D., Bhandari D., Balchakov S., Borchan M.Y., Borch B., Bandari D., Bolchakov S., Borchan M.Y., Borch B., Bandari D., Bolchakov S., Borchan W.Y., Barnel B. W., Bourler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cavley S., Dahlke C., Davengort L.B., Daviss P., M., Cherry J.M., Cavley S., Dahlke C., Davengort L.B., Daviss P., M., Donnes M., Donnes M., Donnes W., Donnes W., Bonnes W., Bornes M., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Bonnes W., Woodage T., Wonser W., Chin W., Smith T., Simpson M., Schoeler F., Shon Y., Smith H.O., Khen Y., Wen W., Zhong W., Zhou X., Zhong W., Zhong W., Zhong W., Zhong W., Zhou X., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Nuclear (Probable).

TISSUE SPECIFICITY: Detected in many cells in the central nervous system, all external sensory organs, some peripheral neurons, and in the non-neural cells of the spiracles and the Malpighian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: Cell-specific pattern of expression. Broadly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed during embryonic development.

DOMAIN: Asn at position 47 of the homeobox may participate in regulating DNA-binding activity by promoting homo- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heterodimerization.
SIMILARITY: Belongs to the CUT homeobox family.
SIMILARITY: Contains 1 homeobox domain.
SIMILARITY: Contains 3 CUT domains.
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tubules.
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274 -----ELDDEBEDEEDEF------DEDDEEENASMQSNADDMELDAQQE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 HVASSAEDDDCANNNTHYSNNNNTSNTATSNT--NNNNNNNSSGGNSEKRKKKNNNNNNG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 PAATVATGAAAAAAAATPIATGNVKSGSTTSNANHT---NSNNSHQDEE------ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 LQQRLGINYLDEFDEFQKEYENALIDYPKKVDGLTDEEDDDGGGLDSIADDEDDDVSYS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 SVDDVGA------DYEDYTD----MLNKLNNAHTGTTPTSETTAEGEGETDS-- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : : | : | : | : | : | 312 TRIEPSATTQQQHQQQDTEDLEENKDAGEASLNVSNNWHNTTDSNNSCSRKNNNGGNESEQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --ASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNE--- 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 PAKATSTATAORRTROLIPLVLGFIGLGLVVAILALTIWOTTRVSHLDKELKSLKRVVDN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 21.8%; Pred. No. 0.6;
Matches 64; Conservative 45; Mismatches 111; Indels 74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 QPAVLLAAKDKEIKALLDELQRLRAQEQTHLVQIQRLEE-----HLEVKRQH 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRH 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetacese; Saccharomyces.
                                                                                                                                                 Nuclear protein; Repeat; Coiled coil.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
CUT 1.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 2175;
                                                                                                                                                                                                                                                                                                                                                                                                                     2124 2136 ALA/PRO-RICH.
2175 AA; 233628 MW; 08BF80C4861BD0AB CRC64;
                                                                                                                                                                                                                                                                                        ALA-RICH.
ASP/GLU-RICH (ACIDIC).
ASN-RICH.
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
ALA-RICH.
HIS/GLN-RICH (OPA-REPEAT).
                                                                                                                                                                                                                    CUT 2.
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
HOMEOBOX.
ALA/GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                        ASP/GLU-RICH (ACIDIC).
ALA/PRO-RICH.
                                                                                                          PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
Transcription regulation; Homeobox; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRO9 protein.
SRO9 OR YCL037C OR YCL37C.
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.3%; Score 137;
                                                                                                                                                                                                                                                                                                                                                                                         ALA-RICH.
             InterPro; IPR007108; Cut homeo.
InterPro; IPR003350; Hmoeo CUT.
InterPro; IPR001356; Homeobox.
                                                 Pfam; PF02376; CUT; 3.
Pfam; PF00046; homeobox; 1.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                    protein;
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1522
1695
1804
210
243
243
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2014
2077
2136
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                                                                                                                                                                                            DNA_BIND
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SEQUENCE FROM N.A.

FlyBase; FBgn0004198; ct. GO; GO:0005634; C:nucleus; IDA.

AE003441; AAF46264.2; EMBL; X07985; CAA30794.1;

PIR; S03170; S03170. TRANSFAC; T02004; -.

4,

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391
160
2229
313
372
308
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                                                                                                                                                                                                                                                     Name=A1;
                                                                                                                                                                                                                                                                             Name=A2;
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CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 VSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSET------TAEGEGETDSASS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 VSTISIEDL-----DATRKKKN--RTPTPKSSTATKWVPIKASITVSGTKRSGSKNG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 ATSKES-----PAPLHHRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMG-- 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 ----YHGDMYIGNDNERNSYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVF 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 ATSOENGOSTOOOOPPHHRNHHHSHH-----HNSNGPORRKFHNSNNAGMPONGGFP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 ASNDDN-----VFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNE
                                                     Kagami M., Toh-B.A., Matsui Y.;
"SRO9, a multicopy suppressor of the bud growth defect in the saccharomyces cerevisiae RHO3-deficient cells, shows strong genetic interactions with tropomyces, suggesting its role in organization of the actin cytoskeleton.";

Genetics 147:1003-1016(1997).

-I- FUNCTION: May overlap in function with tropomycesin and may be involved in organization of actin filaments. Acts as a multicopy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDA BOVIN STANDARD; PRT; 391 AA. Q9BEG5; Q9BEG5; Q9BEG6; 28-FEB-2003 (Rel. 41, Created) 10-OCT-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Ectodysplasin A (Ectodysplasin 1) (Ectodermal dysplasia protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92; Indels
Delgado M., Esteban M., Navas L.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                             466 AA; 51789 MW; AD8BB0895545117C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 134; DB 1;
21.4%; Pred. No. 0.15;
ive 32; Mismatches 92;
                                                                                                                                                                                                                                                                                                                               GO; GO:0005844; C:polysome; IDA.
GO; GO:0003723; F:RNA binding; IDA.
GO; GO:0006412; P:protein biosynthesis; IPI.
InterPro; IPR006630; Lupus_La_dom.
PFART; SM00715; LA; 1.
DOMAIN 200 203 POLY-GIN.
                                                                                                                                                     suppressor of RHO3.
                                            MEDLINE=98043396; PubMed=9383048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 QGD----TPFLQCLNTV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 QQQFYPVQPVLMAINNI 297
                                                                                                                                                                                                                                                                                   EMBL; X59720; CAA42379.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 21.49
                                                                                                                                                                                                                                                                                             PIR; S19365; S19365.
GermOnline; 138873; -.
SGD; S0000542; SRO9.
                                                                                                                                                                                                                                                                                                                                                                                                       203
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taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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EDA BOVIN
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R EMBL; AJ300469; CAC29151.1; JOINED.

R EMBL; AJ300469; CAC29151.1; JOINED.

R EMBL; AJ300469; CAC2915.1.1; JOINED.

R EMBL; AJ300469; CAC2915.1.1; JOINED.

R EMBL; AJ300469; CAC2915.1.1; JOINED.

R EMBL; AJ300469; CAC2915.1.1; JOINED.

R EMBL; AJ300469; CAC2915.1.1; JOINED.

R EMBL; AJ300469; CAC2915.1.1; JOINED.

R EMBL; AJ300469; CAC2915.1.1; JOINED.

R EMBL; AJ300469; CAC2915.1.1; JOINED.

R EMBL; AJ300469; CAC2915.1.1; JOINED.

R EMBL; AJ300469; TNF family.

DR ROSITE; PS00251; TNF 1.

DR PROSITE; PS00251; TNF 2; 1.

RW Differentiation; Developmental protein; Collagen; Transmembrane; KW Signal-anchor; Glycopredin; Alternative splicing.

FT CHAIN 160 391 ECTODYSPLASIN A, MEMBRANE FORM.

FT CHAIN 160 391 ECTODYSPLASIN A, SECRETED FORM.

FT CHAIN 160 391 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 42 62 SIGNALANIOR (TYPE-II MEMBRANE PROTEIN)
                                                                MEDLINE-21070494; PubMed=11167519; Droegemueller C., Distl O., Leeb T.; Droegemueller C., Distl O., Leeb T.; Droegemueller C., Distl O., Leeb T.; Droegemueller C., Distl O., Leeb T.; Droegemueller C., Distl O., Leeb T.; Droegemueller C., Distl O., Leeb T.; Droegemueller C., Distl O., Leeb T.; Anim. Genet. 31:416-416(2000).

-! FWOTION: Probably involved in epithelial-mesenchymal signaling. Isoform Al binds only to the receptor EDAR, while isoform A2 binds exclusively to the receptor XEDAR (By similarity).

-! SUBGELGUIAR LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PTM: N-glycosylated (By similarity).
-!- PTM: N-glycosylated (By similarity).
-!- PTM: Processing by furin produces a secreted form (By similarity).
-!- DISBABE: Defects in EDI are the cause of anhidrotic ectodermal dysplasia. The disease is characterized by sparse hair (atrichosis or hypotrichosis), abnormal or missing teeth and the inability to sweat due to the absence of sweat glands.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
-!- SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).

CLEAVAGE (BY FURIN) (BY SIMILARITY).

COLLAGEN-LIKE.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1F87AD67A04EB7AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ssing (in isoform A2). TId=VSP noras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
-!- ALTERNATIVE PRODUCTS:
    Event-alternative splicing; Named isoforms=2;
    Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sold=Q9BEG5-2; Sequence=VSP_006453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9BEG5-1; Sequence=Displayed;
FROM N.A. (ISOFORMS A1 AND A2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41567 MW;
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                                     264 KARSEDSRPAAHFHLSSRRRHQGS-MGYHGDMYIG--NDNER----NSYQGHFQTRDGVLT 317
                                                              294
                                                                                  318 VINTGLYYVYAQ--ICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIH 375
                                                                                                295 VLVDGTYFIYSQVEVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTN-YNTCYTAGVCL 353
                                                   Bayes M., Hartung A.J., Ezer S., Pispa J., Thesleff I., Srivastava A.K., Kere J., "The anhidrotic ectodermal dysplasia gene (EDA) undergoes alternative splicing and encodes ectodysplasin-A with deletion mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                          ζ
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D; E AND F), AND VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20495245; PubMed=11039935;
Van M., Wang L.-C., Hymowitz S.G., Schilbach S., Lee J., Goddard A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       "X-linked anhidrotic (hypohidrotic) ectodermal dysplasia is caused mutation in a novel transmembrane protein.";
Nat. Genet. 13:409-416(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-Liver;
MEDLINE-98349961; PubMed=9683615;
Monreal A.W., Zonana J., Ferguson B.W.;
"Identification of a new splice form of the EDA1 gene permits
detection of nearly all X-linked hypohidrotic ectodermal dysplasia
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM I), AND VARIANTS EDA HIS-61 AND LEU-69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDA gene in human
                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                          Kere J., Srivastava A.K., Montonen O., Zonana J., Thomas N.S.T., Ferguson B.M., Munoz F., Morgan D., Clarke A., Baybayan P., Chen E.Y., Ezer S., Saarialho-Kere U., la Chapelle A., Schlessinger D.;
                                                                                                                                                                                                            EDA HUMAN STANDARD; PRT; 391 AA. 0926L3; Q976L3; Q976L4; Q978B3; Q976L4; Q978B3; Q976L4; Q976L2; Q976L2; Q976L3; Q976L4; Q1-NOV-1997 (Rel. 35, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Ectodysplasin A (Ectodermal dysplasia protein) (EDA protein).
                 16;
               63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clark S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM A1), AND VARIANTS EDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kobielak K., Kobielak A., Trzciak W.H.; "Expression of a novel transcript isoform of the
                                                                                                                               LERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 409
                                                                                                                                              0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY, AND ALTERNATIVE SPLICING.
28.6%; Prec. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Hum. Genet. Suppl. 7:104-104(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS A1; A2; B; C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR INTERACTION (ISOFORMS A1 AND A2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS A1 AND C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ations.";
J. Hum. Genet. 63:380-389(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum. Mol. Genet. 7:1661-1669(1998).
                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Sweat gland;
MEDLINE=96331280; PubMed=8696334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98409495; PubMed=9736768;
               44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagenous repeats.
  Best Local Similarity
Matches 44; Conserv
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CHÁRACTERIZATION OF VARIANTS CYS-155, CYS-156 AND HIS-156, MUTAGENESIS OF ARC-153; LYS-158 AND ARC-159, AND CLEAVAGE SITE.
MEDILINE-2130995; PubMede-1416205;
Chen Y., Molloy S.S., Thomas L., Gambee J., Baechinger H.P.,
Ferguson B.M., Zonana J., Thomas G., Morits N.P.;
"Mutations within a furin consensus sequence block proteolytic release of ectodysplasin-A and cause X-linked hypohidrotic ectodermal Hum. Mutat. 17:349-349(2001).
-I- FUNCTION: Seems to be involved in epithelial-mesenchymal signaling during morphogenesis of ectodermal organs. Isoform Al binds only to the receptor EDAR, while isoform A2 binds exclusively to the receptor XEDAR. "Scarcity of mutations detected in families with X linked hypohidrotic MEDLINE=21205766; PubMed=11309369; Elomaa O., Pulkkinen K., Hannelius U., Mikkola M., Saarialho-Kere U., VARIANTS EDA CYS-156; HIS-156; CYS-255; ASP-255; GLY-274; TYR-332 AND gene in a ď Paeaekkoenen K., Cambiaghi S., Novelli G., Ouzts L.V., Penttinen M., Kere J., Srivastava A.K.; "The mutation spectrum of the EDA gene in X-linked anhidrotic PROCESSING, MUTAGENESIS OF ARG-153, AND CHARACTERIZATION OF VARIANT MEDLINE=99399307; PubMed=10469321;
MEDLINE=99399307; PubMed=10469321;
Martinez F., Millan J.M., Orellana C., Prieto F.;
"X-linked anhidrotic (hypohidrotic) ectodermal dysplasia caused by novel mutation in EDA1 gene: 406T > G (Leu55Arg).";
J. Invest. Dermatol. 113:285-286(1999). de Vos A.M., Gao W.-Q., Dixit V.M.; "Two-amino acid molecular switch in an epithelial morphogen that "Ectodysplasin is released by proteolytic shedding and binds to ď VARIANTS EDA ARG-60; TYR-252; VAL-269; SER-302 AND MET-378.
MEDLINE=21272350; PubMed=11378824;
Vincent M.C., Biancalana V., Ginisty D., Mandel J.L., Calvas E "Mutational spectrum of the EDI gene in X-linked hypohidrotic Ferguson B.M., Thomas N.S.T., Munoz F., Morgan D., Clarke A., Hertz J.M., Noergaard Hansen K., Juncker I., Kjeldsen M., Gregersen N.; em inseense mutation (402C--xT) in exon 1 in the EDA family with X-linked hypohidrotic ectodermal dysplasia."; clin. Genet. 53:205-209(1998). Proc. Natl. Acad. Sci. U.S.A. 98:7218-7223(2001). ectodermal dysplasia: diagnostic implications."; J. Med. Genet. 35:112-115(1998). regulates binding to two distinct receptors."; Science 290:523-527(2000). J. Hum. Genet. 9:355-363(2001) Mol. Genet. 10:953-962(2001). MEDLINE=21193173; PubMed=11295832; VARIANT EDA TYR-54. MEDLINE=98292028; PubMed=9630076; VARIANT EDA LYS-63. MEDLINE=98168231; Pubmed=9507389; ectodermal dysplasia."; ectodermal dysplasia." protein." dysplasia

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us-09-813-329-6.rsp

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264 KARSEDSRPAAHFHLSSRRRHQGS-MGYHGDMYIG--NDNER---NSYQGHFQTRDGVLT 317
                                                                                                                                                        240 KAGTRENOPAV-VHLOG----OGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELE 294
                                                                                                                                                                                                            318 VINTGLYYVYAQ--ICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIH 375
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-mib.ch/announce/or send an email to license@isb-mib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97313267; PubMed=9169871; Johnston M., Andre B., Ansorge W., Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brucekner M., Delius H., Dubois E., Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis B.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Moeller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Redhemn S., Rieger M., Rinke M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Veterndeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Medler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D., M. T., A., Andelse Sequence of Saccharomyces cerevisiae chromosome XII., M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 387:87-90(1997).
-1- FUNCTION: Controls the pre-rRNA processing machinery in conjunction with FHL1. Could convert FHL1 from a repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cherel I., Thuriaux P.; "The IFH1 gene product interacts with a fork head protein in
        Score 132; DB 1; Length 391;
Pred. No. 0.17;
                                                            Indels
                                                            63;
                                                                                                                                                                                                                                                                                                                    LERNERIHLKDIHNDRNAVLREGNNRSYFGIFKV 409
                                                                                                                                                                                                                                                                                                                                                     |: ::| :| :| : : ::|| :: 354 LKARQKIAVKWVHADIS--INMSKHTTFFGAIRL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1085 AA
                                                      31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FH1 protein (RRP3 protein).
FH1 OR RRP3 OR YLR223C OR L8083.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 28383 / FL100;
MEDLINE-95304839; PubMed-7785326;
        6.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z29488; CAA82624.1; -.
EMBL; U19027; AAB67412.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae.";
Yeast 11:261-270(1995).
                                                   44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S55352; S55352.
GermOnline; 142285; -.
SGD; S0004213; IFH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to an activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEAST
Query Match
Best Local S
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                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: N-glycosylated.

PTM: N-glycosylated.

PTM: Processing by furin produces a secreted form.

DISBASE: Defects in EDI are the cause of ectodermal dysplasia, anhidrotic (EDA) [MIM:305100] also known as X-linked hypohidrotic ectodermal dysplasia (XLHED). EDA is a disease characterized by sparse hair (atrichosis or hypotrichosis), abnormal or missing teeth and the inability to sweat due to the absence of sweat glands. EDA is the most common form of over 150 clinically distinct ectodermal dysplasias. This disease was already described
                                                                                                                                                                                                                                                                                                                         Isold=Q92838-8; Sequence=VSP 006460, VSP 006461;
TISSUE SPECIFICITY: Not abundant; expressed in specific cell types
of ectodermal (but not mesodermal) origin of keratinocytes, hair
                                                                                                                                                                                                                                                                                                                                                                                                      follicles, sweat glands. Also in adult heart, liver, muscle, pancreas, prostate, fetal liver, uterus, small intestine and umbilical chord.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SÍMILARITY: Belongs to the tumor necrosis factor family. SIMILARITY: Contains 1 collagenous domain.
                                                                                                                  IsoId=Q92838-4; Sequence=VSP_006462, VSP_006463;
                                                                                                                                                                   IsoId=092838-5; Sequence=VSP_006458, VSP_006461;
             Isoid=092838-2; Sequence=VSP_006454, VSP_006455;
                                                                                                                                                                                                                    Bold=Q92838-6; Sequence=VSP_006456, VSP_006457;
                                                                                                                                                                                                                                                                                   VSP_006461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005856; C:cytoskeleton; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:00071398; P:ectoderm development; TAS.
GO; GO:0007158; P:signal transduction; TAS.
InterPro; IPR008160; Collagen.
InterPro; IPR008163; TNF Emniy.
InterPro; IPR00893; TNF_like.
                                                                                                                                                                                                                                                                        IsoId=Q92838-7; Sequence=VSP_006459,
                                      Name=A2;
IsoId=Q92838-3; Sequence=VSP_006464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF060999; AAC36302.1; ---
AF060999; AAC36303.1; ---
AF060992; AAC36303.1; ---
AF060994; AAC36303.1; JOINED.
AF060995; AAC36303.1; JOINED.
AF060995; AAC36303.1; JOINED.
AF060995; AAC36303.1; JOINED.
AF060995; AAC36303.1; JOINED.
AF060995; AAC36303.1; JOINED.
AF060995; AAC36303.1; JOINED.
AF060995; AAC36303.1; JOINED.
AF1580699; CAD18890.1; ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF061192; AAC77374.1; -. AF061193; AAC77375.1; -. AF061194; AAC77376.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL158141; CAD13493.1; -. Senew: HCMC.3157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U59227; AAC50678.1; -. U59228; AAC50679.1; -.
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MIM; 300451

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12;
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                                                                                                                                                                                                                                                                                              262 ISFGNGNEGYNEDIGEEVLDLKOKENNGNEEDKLDSKVMLGNNDELRFPNISESDESE-- 319
                                                                                                                             KELKSLKRVVDNLQQRLGINYLDEFDEFQ-----KEYENALIDYPKKVDGLTDEEDDDDG 123
                                                                                                                                                    KKSKLIQRQIDNDDEG-----TESSDYQAVTDGEESENEEEESEEEEDDEDDDDDD 147
                                                                                                                                                                                                                                                                             197 TSY-NAHKKKQERKSRSIADVRNEEQN------IQGNHTELQEKSSNEATSKESP 244
                                                                                                                                                                                                                                                                                                                                                       ------YDIDQDAYPDVINNEDSHGEIGTDLETGEDDLPILEE 356
                                                                                                                                                                                                                                                                                                                                                                                300 NERN------SYQG--HFQTRDGVLTVTNTGLYYVYAQ-ICYNNSHDQNGFIVFQ 345
                                                                                                                                                                                                                                                                                                                                                                                                       357 EEQNIVSELQNDDELSFDGSIHEEGSDPVEDAENKFLQNEYNQENGYDEEDDEEDEIMSD 416
                                                                                                                                                                                                                             161 NAHTGTTPTSETTAE--------GEGETDSASSASNDDNVFDDF
                                                                                                                                                                                                                                              245 APLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMGY-----HGDMYIGND
                                                                                                                                                                                                    DGSDSDSDS-----TSSDDENIDFVKLTAQRKKRAMKALSAMNTNSNTLYSSRENSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM TAD).
MEDILTE=9749104; PubMed=9285798;
FERGHUSON B.M., Brockdorff N., Formetone E., Ngyuen T.,
Kronmiller J.E., Zonana J.;
"Cloning of Tabby, the murine homolog of the human EDA gene: evidence
for a membrane-associated protein with a short collagenous domain.";
Hum. Mol. Genet. 6:1589-1594(1997).
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kere J., Schlessinger D.;
"The Tabby phenotype is caused by mutation in a mouse homologue of "The Tabby phenotype is caused by mutation in a mouse and encodes a protein (ectodysplasin-A) with collagenous domains.";
Proc. Natl. Acad. Sci. U.S.A. 94:13069-13074(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=129/Sv;
MEDLINE=98058770; PubMed=9371801;
Srivaetava A.K., Pispa J., Hartung A.J., Du Y., Ezer S., Jenks T., Srivaetava A.K., Pispa J., Hartung A.J., Ko M.S.H., Thesleff I., Shimada T., Pekkanen M., Mikkola M.L., Ko M.S.H., Thesleff I., Kere J., Schlessinger D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                    48; Mismatches 126; Indels 120;
                                                                            DB 1; Length 1085;
GO; GO:0006348; P:chromatin silencing at telomere; IMP. GO; GO:0006364; P:rRNA processing; IGI. Nuclear protein; Transcription regulation.

DOMAIN 122 163 ASP/GLU-RICH (HIGHLY ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDA MOUSE STANDARD; PRT; 391 AA.
054693; O35705; Q9QMU8; Q9QZ01; Q9QZ02;
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ectodysplasin A (EDA protein homolog) (Tabby protein).
Mus musculus (Mouse).
                                                  1085 AA; 122491 MW; BEIC7DEF06213FE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS TAA; TAB AND TAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS TA-A2 AND TA-A3).
                                                                                       0.85;
                                                                            6.0%; Score 129;
                                                                                        Pred. No.
                                                                                        19.98;
                                                                                                    73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                GDTPFLQ 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                        417 FÖMPFYE 423
                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     # MORESTORM FOR THE PROPERTY OF CELL; IDA.

GO:0045177; C:apical part of cell; IDA.
GO:0005789; C:andoplasmic reticulum membrane; IDA.
GO:0005897; C:integral to plasma membrane; IDA.
GO:0007160; P:cell-matrix adhesion; IDA.
GO:0042346; P:positive regulation of NF-kappaB protein-nu. . ; IDA.
GO:0007411; P:salivary gland development; IDA.
                                                                                                             "Ectodysplasin, a protein required for epithelial morphogenesis, is a novel TNF homologue and promotes cell-matrix adhesion."; Mech. Dev. 88:133-146 (1999).

-!- FUNCTION: Involved in epithelial-mesenchymal signaling during morphogenesis of ectodermal organs. Isoform TRA binds only to the receptor EDAR, while isoform TA-A2 binds exclusively to the receptor XEDAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PTM: N-glycosylated (By similarity).
-!- PTM: N-glycosylated (By similarity).
-!- PTM: Processing by furin produces a secreted form (By similarity)
-!- DISEARE: Defects in ED1 are the cause of the tabby phenotype in mice (the equivalent of anhidrotic ectodermal dysplasia in humans). The disease is characterized by sparse hair (atrichosis or hypotrichosis), abnormal or missing teeth and the inability to sweat due to the absence of sweat glands.
                                         P., Kere J.,
                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Homotrimer (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Differentiation, Developmental protein, Collagen, Transmembrane, Signal-anchor, Glycoprotein, Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the tumor necrosis factor family.
MEDLINE=20005791; Pubmed=10534613;
Mikkola M.L., Pispa J., Pekkanen M., Paulin L., Nieminen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=O54693-3; Sequence=VSP_006469, VSP_006471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=054693-5; Sequence=VSP_006465, VSP_006468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=6;
Comment=Additional isoforms seem to exist;
Name=TAA; Synonyms=Al;
IsoId=054693-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=054693-4; Sequence=VSP_006466,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=054693-6; Sequence=VSP 006470;
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EMBL; AF016629; AAB95203.1; --
EMBL; AF016630; AAB95203.1; --
EMBL; AF016630; AAB95205.1; --
EMBL; AF016631; AAB95206.1; --
EMBL; AF004435; AAB98122.1; --
EMBL; AF004435; AAB88122.1; --
EMBL; AJ24365; CAB73849.1; --
EMBL; AJ243659; CAB73849.1; --
EMBL; AJ243659; CAB73849.1; --
EMBL; AJ243659; CAB72696.1; --
EMBL; AJ243659; CAB72697.1; --
EMBL; AJ243659; CAB7261 part of
GO; GO:0005897; C:integral to pla
GO; GO:0001589; C:integral to pla
GO; GO:0001431; P:ealiwary gland
GO; GO:0001446; P:ealiwary gland
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InterPro; IPR006052; TWF family.
InterPro; IPR008983; TWF like.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=TA-A3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
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STANDARD;
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116 1
278 AA;
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                                                                                                                                                                                                                                                                                                                                                      264 KARSEDSRPAAHFHLSSRRRHQGS-MGYHGDMYIG--NDNER---NSYQGHFQTRDGVLT 317
                                                                                                                                                                                                                                                                                                                                                                  | : :::|| || || || 240 KTGTRENQPAV-VHLQG----QCSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELE 294
                                                                                                                                                                                                                                                                                                                                                                                          318 VTNTGLYYVYAQ--ICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIH 375
                                                                                                                                                                                                                                                                                                                                                                                                     295 VLVDGTYFIYSQVEVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTN-YNTCYTAGVCL 353
                                                                                                    MALLINFFFPDEKAYSEEESRRVRRNKRSKSGEGADGPVKNK
KKGKKAGPPGPNGPPGPPGPPGPPGPPG1PG1PG1PGTTVM
                                                                                                                       GPPGPPGPPGPPGLQGPSGAA -> VSHLGGAAALEAP
                                                                                                                               SPARLGGGLGLRAQGTLPLRAKFQGRSWEWAGVLGRGCPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Endometrium;
MEDLINE=99423513; PubMed=10491620;
Johnson G.A., Spencer T.E., Burghardt R.C., Bazer F.W.;
Johnson G.A., Choring and expression of messenger ribonucleic acid in the uterus during the periimplantation period.";
Biol. Reprod. 61:884-891(1999).
                                                                                                                                                          /FTIG=VSP_006465.

PVENTKKKER -> KSTQVIFFP (in isoform TAB).
/FTIG=VSP 006466.
Missing (in isoform TAB).
Missing (in isoform TAB).
Missing (in isoform TAC).
/FTIG=VSP_006467.
                             CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                        VVLGSCLGSSRPSPVPWSWKAQPARAAPGEVWAA (in
                                                                                                                                                                                                                                                           Missing (in isoform TA-A2 and isoform
                                                            COLLAGEN-LIKE.
CLEAVAGE (BY FURIN) (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
...THYPH (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                      16;
 ECTODYSPLASIN A, MEMBRANE FORM ECTODYSPLASIN A, SECRETED FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                    Score 128; DB 1; Length 391; Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                   43; Conservative 31; Mismatches 64; Indels
                                                                                                                                                                                                                        (in isoform TA-A3).
                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                  /FTId=VSP 006469.
Missing (in isoform TAD).
                                                                                                                                                                                                                                                                             /FTIG=VSP 006471.
7-x E (IN REF. 2).
ESECEDASBD60DEFF CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Osteopontin precursor (Bone sialoprotein 1).
SPP1 OR OPN.
Ovis aries (Sheep).
                   SIMILARITY)
                                                                                                                                                   isoform TAC
                                                                                                                                                                                                                                                     FTIG=VSP
                                                                                                                                                                                                                         Missing
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41603 MW;
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62
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391 AA;
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                                                     63
180
159
313
372
133
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TRANSMEM
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CARBOHYD
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                                                     DOMAIN
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Q9XS<u>Y</u>9;
CHAIN
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PROSITE; PS00884; OSTEOPONTIN; 1.

Cytokine; Glycoprotein; Stalic acid; Biomineralization; Cell adhesion; Phosphorylation; Signal.

By SIMILARITY.
                                                                              FUNCTION: Acts as a cytckine involved in enhancing production of interferon-gamma and interleukin-12 and reducing production of interleukin-10 and is essential in the pathway that leads to type I immunity (By similarity).

SUBUNIT: Ligand for integrin alpha-V/beta-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 VLGFIGLGLVVAILALTIWQTTRVSHLDKELKS------LKRVVDNLQQRLGINYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYEDYTDMINKLNNAHTGTTP-TSETTAEGEGETDS------ASSASNDDNVFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 VICFCLLGIA---SALPVKPISSGSSEEKOLNNKYPDAVATWLKPDPSOKOTFLEPQNSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHS
FUNCTION: Binds tightly to hydroxyapatite. Appears to form an integral part of the mineralized matrix. Probably important to cell-matrix interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47;
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                                                                                                                                                                                                                                                                          -1- PTM: Extensively phosphorylated on serine residues (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 123.5; DB 1; Length 23.3%; Pred. No. 0.38; ive 37; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37D49E1DD1FBFD47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OSTEOPONTIN.
CELL ATTACHMENT SITE.
N-LINKED (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                                                        -1- PTM: N- and O-glycosylated (By similarity).
-!- SIMILARITY: Belongs to the osteopontin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Zinc finger protein 265 (Zinc finger, splicing).
ZNF265 OR ZIS.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF152416; AAD38388.1; -...GO; GO:0005576; C:extracellular; ISS. GG: GO:0005125; F:cytckine activity; ISS. InterPro; IPR002038; Osteopontin. Pfam; PF00865; Osteopontin; I...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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PDB; 1EJ7; 16-OCT-00.
PDB; 1FJC; 16-OCT-00.
INDB; 1FJC; 03-JAN-01.
INTERPRO; 1FR000564; RNA_rec_mot.
Pfam; PF00076; rrm; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-X
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                                                    NCBI_TaxID=10036;
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstarion the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 KRVVD-----NLQQRLG-----INYLD-----EFDEFQKEYENALIDYPKKVDG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---LTDEEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRNEEQNIQGNHTEL 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253
: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Karginova E.A., Pentz E.S., Kazakova I.G., Norwood V.F., Carey R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 QEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMG
                                                                                                            "Zis: a developmentally regulated gene expressed in juxtaglomerular
                                                                                                                                 Am. J. Physiol. 273:F731-F738(1997).
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- TISSUE SPECIFICITY: Expressed in Kidney; more specifically renal juxtaglomerular (GG) cells.
-!- SIMILARITY: Contains 2 RANBP2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90D6C7C3DE3A658F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
NucleoIn (Protein C23).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 0.47;
46; Mismatches
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RANBP2-TYPE 2.
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20.4%; Pred. No. 0.4
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                                                             STRAIN=Sprague-Dawley; TISSUE=Kidney;
MEDLINE=98042249; PubMed=9374836;
                                                                                                                                                                                                                                                                                                                                                                                                                   Zinc-finger; Nuclear protein; Repeat.
                                                                                                                                                                                                                                                                                                              EMBL; AF013965; AAC02295.1; -... EMBL; AF013966; AAC02296.1; -... EMBL; AF013967; AAC02297.1; -... InterPro; IFR001876; Znf RanGDP. Pfam; PF00641; zf-RanBF; 2... PRART; SM00647; ZnF RBZ; 2... PRGSITE; PS01358; ZF RANBP2.1; 2... PROSITE; PS0199; ZF-RANBP2.2; 2... PROSITE; PS0199; ZF-RANBP2.2; 2...
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198 262 AJ
332 AA; 37837 MW;
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Best Local Similarity 20.4
Matches 61; Conservative
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  Eukaryota; Metazoa;
                                                SEQUENCE FROM N.A.
                    NCBI_TaxiD=10116;
                                                                                                  Gomez R.A.;
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P08199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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ASP/GLU-RICH (ACIDIC).
RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 4.
ARG/GLY/PHB-RICH.
8 X 8 AA TANDEM REPEATS OF X-T-P-X-K-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lapeyre B., Bourbon H., Amalric F.;
"Nucleolin, the major nucleolar protein of growing eukaryotic cells:
an unusual protein structure revealed by the nucleotide sequence.";
Proc. Natl. Acad. Sci. U.S.A. 84:1472-1476(1987).
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PROSITE; PS50102; RRM; 4.
PROSITE; PS00030; RRM RNP 1; 3.
Nuclear protein; Phosphorylation; Methylation; DNA-binding; Repeat;
RNA-binding; 3D-structure.
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Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomí;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erard M.S., Belenguer P., Caizergues-Ferrer M., Pantalon1 A.,
Amalric F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A major nucleolar protein, nucleolin, induces chromatin
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                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 35-713 FROM N.A., AND SEQUENCE OF 1-34 MEDLINE=87175501; PubMed=3470736;
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MEDLINE=88312631; PubMed=3409881;
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PRT;
                                                                          EMBL; Y07893; CAA69201.1; -. EMBL; Z73055; CAA97300.1; -. EMBL; X81072; CAA56963.1; -.
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1016
11142
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1016
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                                                                                                                                                                                                                                            98 KEYENALIDYPKKVDGLTDEEDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLN 157
                                                                                                                                                                                       158 KLNNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNA-----HKKKQER-- 208
                                                                                                                                                                                                           171 PVVKGKQGKVAAAAPASEDEDEEEDEEEEEDDEEEEDDSEEEEAMEITPAKGKKAPAKVV 230
                                                                                                                                                                                                                                --KSRSIADVRNEEQNIQGNHTELQEKSSNEATSKE----SPAPLHHRRRMHSRHRH 259
                                                                                                                                                                                                                                                                                           291 PEAKKOKVEGSESTTPFNL--------FIGNLNPNKSVAELKVAISEPFAKN 334
                                                                                                                                                                                                                                                                        260 LLVRKARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNERNS-----YQGHFQTR 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95274317; PubMed=7754704; Schnall R., Mannhaupt G., Stucka R., Tauer R., Ehnle S., Schwarzlose C., Vetter I., Feldmann H.; "Identification of a set of yeast genes coding for a novel family putative ATPases with high similarity to constituents of the 26S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
Agostoni Carbone M.L., Lucchini G., Melchioretto P., Nardese V., Vanoni M., Panzeri L.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                             63;
                                                                                                        DB 1; Length 713;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                  79DDCF724CED7DB4 CRC64;
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                                                                                                                            40; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   procease complex.";
Yeast 10:1141-1155(1994)
-!- SIMILARITY: Belongs to the AAA ATPase family
-!- SIMILARITY: Contains 1 bromodomain.
                                (DI-)
                                                    (DI-).
                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
YTAT-binding homolog 7.
                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1379 AA
                                                                                                      5.7%; Score 122.5;
20.0%; Pred. No. 1.3
  METHYLATION
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                                                                                                                                                                                                                                                                                                                  DGVLTVTNTGLYYVYAQICYNNSHD 337
                                                                                  76997 MW;
                                                                                                                          53; Conservative
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   665
669
673
679
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681
                                                                                                     Query Match
Best Local Similarity
                                                                                  713 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
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Feldmann H.;
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TBP7_YEAST
ID TBP7_YEAST
AC P40340;
                                                                     MOD_RES
SEQUENCE
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23.8%; Pred. No. 2.9;
tive 40; Mismatches 101;
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GermOnline; 141582; -
SGD; S0003502; YTA7.
InterPro; IPR003959; AAA_ATPase.
InterPro; IPR003959; AAA_ATPase.
InterPro; IPR003969; AAA_ATPase.
InterPro; IPR001360; AAA_Bub.
InterPro; IPR001407; Bromodomain.
Pfam; PF00409; Dromodomain, 1.
Pfam; PF00409; Dromodomain; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00674; AAA; 1.
PROSITE; PS00674; AAA; 1.
PROSITE; PS00674; AAA; 1.
PROSITE; PS00674; BROWDOWAIN 1; FALSE NEG.
PROSITE; PS00014; BROWDOWAIN 2; 1.
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Actaubherg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S.W., Worley D.M., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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location, and RPLP analysis of human osteopontin (OPN).";
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  Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Crosby A.H., Edwards S., Murray J.C., Dixon M.J.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=95139605; PubMed=7837791;
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Lab. Invest. 72:55-63(1995).
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                       NCBI_TaxID=9606;
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Here. Natl. Aadd. Scil. U.S.A. 9916899-16801(2002).

Proc. Natl. Mand. Scil. U.S.A. 9916899-16801(2002).

Representation of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of th
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                                                           Cytokine; Glycoprotein; Sialic acid; Biomineralization; Cell adhesion; Phosphorylation; Signal; Alternative splicing; Polymorphism. SIGNAL 1 16 POTENTIAL.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
Zinc finger protein 265 (Zinc finger, splicing) (Fragment)
Mus musculus (Mouse).
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R -> H (in dbSNP:4660).

/FTId=VAR 014717.

D -> H (IN REF. 7).

T -> A (IN REF. 7).

SHEF -> GNSL (IN REF. 2).
                                                                                                               4996429EC4752B86 CRC64;
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MLVVDPKSKBEDK-----HLKFRISHE 305
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MEDLINE-20237530; Pubmed=10773668;
                                               PROSITE; PS00884; OSTEOPONTIN; 1
Pfam; PF00865; Osteopontin; 1.
          PRINTS; PRO0216; OSTEOPONTIN.
SMART; SM00017; OSTEO; 1.
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MEDLINE=99132651; PubMed=9931435;
Nakano M., Yoshiura K., Oikawa M., Miyoshi O., Yamada K., Kondo S.,
Miwa N., Soeda E., Jinno Y., Fujii T., Niikawa N.;
"Identification, characterization and mapping of the human ZIS (zincfinger, splicing) gene.";
Gene 225:59-65(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 QEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMG
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
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MEDINE-21154917; PubMed-11230166;
Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36739 MW; 94593499E481FE88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 ----EDEDEDDADLSKYN----LDASEEEDSNKKKSNRRSRS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z265 HUMAN STANDARD; PRT; 337 AA. 095218; Q9UP63; CCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Zinc finger protein 265 (Zinc finger, splicing). ZNF265 OR ZIS.
                                                                                                                                                                                                    EMBL; AF133818; AAF04474.1; -.
MGD; MGI:1858211; Zfp265.
InterPro; IRR001876; Znf RanGDP.
Pfam; PF00641; Zf-RanBp; 2.
SWART; SM00547; ZnF RBZ; 2.
PROSITE; PS01388; ZF-RANBP2 1; 2.
PROSITE; PS01389; ZF-RANBP2 2; 2.
ZinC-finger; Nuclear protein; Repeat.
ZN_FING 9 40 RANBP2-TYPE 1.
ZN_FING 65 94 RANBP2-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.6%; Score 121.5; DE 20.4%; Pred. No. 0.62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARG/SER-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 KRVVD-----NLQQRLG-----INYLD-----EFDEFQKEYENALIDYPKKVDG 113
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Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaler B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.;

"Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";

el. SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.6%; Score 121; DB 1; Length 337; 20.2%; Pred. No. 0.69; ive 47; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VSP 004493.
337 AA; 38223 MW; A4D20F6B3AD95925 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIN; O:0138.; G. mucleus; TAS. GO; GO:0003723; F.RNA binding; TAS. GO; GO:0003700; F.transcription factor activity; TAS. GO; GO:0008380; P:RNA splicing; TAS. InterPro; IPRO1875; ZAF_RANGDP.
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SIMILARITY: Contains 2 RANBP2-type zinc fingers.
                                                                                                                                                       Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isoform ZIS-2
                                                                                                                                                                       Name=ZIS-1;
IsoId=095218-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF065391; AAD09746.1; -. EMBL, AF065392; AAD09747.1; -. EMBL, ALL18945; CAB66879.1; -. Genew, HGNC:13058; ZNF265.
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Job time : 14 secs

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1 MTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV 409
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        Q81E75
        Q81Z74
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        6.8
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        21
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        6.8
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ID 01-OCT-2002 (TrEMBLrel. 22, Created)

ID 01-OCT-2002 (TrEMBLrel. 25, Last sequence update)

ID 01-OCT-2002 (TrEMBLrel. 25, Last sequence update)

IN 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

IN 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

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IN 020-OCT-2003 (TREMBLRel. 25, Last sequence update)

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Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22775938; PubMed=12894227;
Sutuppila S., Maaty W.S., Chen P., Tomar R.S., Eby M.T., Chaj
Chew S., Rathore N., Zachariah S., Sinha S.K., Abrams J.M.,
Chaudhary P.N.,
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Moreno E., Yan M., Basler K.;
"Evolution of TNF Signaling Mechanisms. JNK-Dependent
"Triggered by Eiger, the Drosophila Homolog of the TNF
Curr. Biol. 12:1263-1268 (2002).
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Last annotation update)
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          0; Mismatches
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EIGER OR CG12919 OR DARTH.
          Conservative
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Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
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     8306AECCE14397B8 CRC64;
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                                           100.0%; Score 2162; DB 5;
ilarity 100.0%; Pred. No. 1.4e-136;
Conservative 0; Mismatches 0;
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Pred. No. 3.1e-136;
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RECENCE G.G., Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,

Recorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Recorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Record R.C., Rogers Y.-H.C., Blazej R.G., Chan L.X.,

Randon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Mikhos G.L.G.,

Ran K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikhos G.L.G.,

Ran K.H., Boyle C., Baxter B.G., Helt G., Nelson C.R., Mikhos G.L.G.,

Rallew R.M., Basu A., Baxter B.G., Helt G., Nelson C.R., Baldwin D.,

Resson K.Y., Benos P.V., Berman B.P., Bandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Ruttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Roslow K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Roslor K., Gabrielian A.E., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,

Roslor C., Gabrielian A.E., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,

Roslor C., Gabrielian A.E., Gorrell J.H., Gu Z., Gener J., Harris M.,

Roslor M., Howland T.J., Wei M.-H., Ibegwam C.,

Ran Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Rannel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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                                                                                             MTAETLKPFITPTSANDDGFPAKATSTATAQRRTRQLIPLVLGFIGLGLVVAILALTIWQ
                                                                                                                                                TTRVSHLDKELKSLKRVVDNLQQRLGINYLDEFDEFQKEYENALIDYPKKVDGLTDEEDD
                                                                                                                                                                                                         DGGGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTAEGEGET
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                                                                                                                                                                                                                                                                                                                               MTAETLKPFITPTSANDDGFPAKATSTATAQRRTRQLIPLVLGFIGLGLVVAILALTIWQ
                                                                                                                                  TTRVSHLDKELKSLKRVVDNLQQRLGINYLDEFDFFQKEYENALIDYPKKVDGLTDEEDD
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                                                                                                                                                                                                                                                                                                              KESPAPLHHRRRMHSRHRHLLVRK-----ARSEDSRPAAHFHLSSRRRHQGSMGYHGDM
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Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
            Length 415;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
          Query Match 99.4%; Score 2149; DB 5; Best Local Similarity 98.6%; Pred. No. 1.1e-135; Matches 409; Conservative 0; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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EIGER OR CG12919.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 INNAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRN 128
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EIGER OR CG12919.

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilae; Drosophila.

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                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 325 AA; 36862 MW; 6ESCCB69694F1A3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.6%; Score 1656; DB 5; 97.8%; Pred. No. 7.1e-103; ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 97.8
Matches 310; Conservative
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Pain A., Berriman M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRK-----ARSE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIH 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Change M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Parel S., Phouanenavong S., Man K., Yu C., Lewis S.E., Rubin G.M.,
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MEDLINE=99376085; PubMed=10448855;
MEDLINE=99376085, PubMed=10448855;
Churcher C.M., Lawson D., Babham D., Brown D., Chillingworth T., Churcher C.M., Craig A., Davies R.M. Devlin K., Feltwell T., Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Rutter S., Skelton J., Squares R., Squares S., Sulston J.E., Whitehead S., Woodward J.R., Newbold C., Barrell B.G., "The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                62.9%; Score 1359; DB 5; Length 261; 97.7%; Pred. No. 3.8e-83; ive 0; Mismatches 0; Indels 6
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Eukaryota<u>;</u> Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
SEQUENCE 261 AA; 29780 MW; 13B6D5A04EC9122C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 23, Last sequence update) (TrEMBLrel. 24, Last annotation update)
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MEDLINE=222555708; PubMed=12368867;
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Best Local Similarity
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                  Mungall K., Bowman S., Arkin R., Baker S., Barron A., Brothe B.,

Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

Chillingworth T., Christodoulou Z., Clark E., Corton C.,

Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,

Relevell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,

Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,

Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

A. Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,

A. Oliver K., Ormond D., Price C., Quail M.A., Rabbinowitsch E.,

Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,

Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,

A. Stlston J.B., Craig A., Newbold C., Barrell B.G.,

Sulston J.B., Craig A., Newbold C., Barrell B.G.,

T. Sequence Of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 D--DDYDDEDDDD----YEDDDD-----DDYDDDEDNYNNSYDNGYNTKHNKKKINPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 LSISNDHIEKEN--NLYIQNEQFINYDDVIFRKFK------FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 SSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRN-----EEQNIQGNHTELQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 YNSTIFETSNMNFCVKDEKRKKEKOKNSI-DKRNIIYSDDBSDNNYEHIFTHINSDLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 -KSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGSMGYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 GDMYIGNDNER-----NSYQGHFQTRDGVLTVTNTGLYYV---YAQI--CYNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 HDQNGFIVFQGDTPFL-----QCLNTVPTNMPHKVHTCHTSGLIHLERNERIHLKDIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85; Gaps
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BEDLINB-22555708 PubMed=12368867;
Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D., Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2226;
      Harris
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
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Last annotation update)
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21.9%; Pred. No. 0.0062;
ive 57; Mismatches 150;
Churcher C.,
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EMBL, AL034558; CAB38989.3; -.
InterPro. IPR007259; Spc97_Spc98.
Pfam; PF04130; Spc97_Spc98; 1.
Hypothetical protein.
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Hypothetical protein.
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Q03280;
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Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,

A Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,

Cronin A., Davies R., Davies P., Dear P., Deagett J.,

Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,

Humphrey D., Haueer H., Hornsby T., Holroyd S., Horrocks P.,

Humphrey S., Jagels K., James K.D., Johnson D., Kerhornon A.,

Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

A ine A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,

Oliver K., Ormond D., Price C., Quall M.A., Rabbinowitsch E.,

A Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,

Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,

Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,

Sulscon J. E., Craig A., Newbold C., Barrell B.G.

"Sequence of Plasmodium falciparum chromosomes I, 3-9 and 13.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 TELQEKSSNEATSKESPAPLHHRRRMHSRHRHLLVRKARSEDSRPAAHFHLSSRRRHQGS 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :: || : || : || |: || 523 ASDMYNKDTN-MSSLNTSENTLPLYIILDCSAVLDMKELWKDKSILPFSFPGLLYLYLNNK 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 MGYHGDMYIGNDNERNSYQGHFQ--TRDGVLTVTNTGLYYVYAQICYNNSHDQNGFI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNYNNNNNINNNNNNNNNKKKSNLVKDKKNSSTSTCNKFM-----NNTHNLNKSFSNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 LDKELKSL----KRVVDNL----QQRLG--INYLDEFDEFQKEYENALIDYPKKVDGLTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 EEDDDDGDGLDSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTAEG
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MEDLINE=22255708; PubMed=12368867;
Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 2221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.0%; Score 172.5; DB 5; Length; Best Local Similarity 21.2%; Pred. No. 0.0099; Matches 83; Conservative 61; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2221 AA; 255042 MW; 7311E1373C1B6E44 CRC64;
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Last annotation update)
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EMBL; AL031745; CAD49042.1; -.
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Pfam; PF00849; PseudoU synth_2; 1.
PROSITE; PS00199; CYTOCHROWE C; 1.
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PROSITE; PS00144; MATH; 1.
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 YNAHKKKQERKSRSIADVRNEEQNIQGNHTELQE-------KSSNEATSKES
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01-NOV-1996 (TrEMBLral. 01, Created)
01-NOV-1996 (TrEMBLral. 01, Last sequence update)
01-OCT-2003 (TrEMBLral. 25, Last annotation update)
01-OCT-2003 (TrEMBLral. 25, Last annotation update)
08035.1P (Ubiquitin ligase).
TCM1 OR D8035.1 OR YDR457W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomyces.
Saccharomycetales; Saccharomycetaes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 165.5; DB 3; Length 3268;
; Pred. No. 0.046;
66; Mismatches 142; Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ucsugi T., Kikuchi Y.;
Ucsugi T., Kikuchi Y.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U33050, AAB64910.1;
EMBL; U33050, BAA21482.1;
EMBL; U53005; S6625,
SGD; S0002865; TOWL
GO; GO:0007067; P:mitcsis; IMP.
GO; GO:0006937; P:muclear organization and biogenesis; IMP.
GO; GO:0006913; P:mucleocytoplasmic transport; IMP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jia Y., Cherry J.M.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR000569; HECT_domain.
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Matches 78; Conservative 6
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1254 RYTTLSSSFLPSSEASVNDSAXNDYKDDIYNNKKEKIEELKSDEKAFNTTETNCSONKII 1313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=207;
MEDLINE=2255705; PubMed=12368864;
MEDLINE=2255705; PubMed=12368864;
MEDLINE=2255705; PubMed=12368864;
MEDLINE=2255705; PubMed=12368864;
MATHON J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Elsen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S., Pertea M., Allen J., Selangut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B., Hoffman S.L., Newbold C., Davis R.W., "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 TDEEDDDDGGLGSIADDEDDDVSYSSVDDVGADYEDYTDMLNKLNNAHTGTTPTSETTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.6%; Score 164; DB 5; Length 2026; 22.2%; Pred. No. 0.033; ive 64; Mismatches 123; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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                                       2165 QSNLINPLGPTGLEQVENDISDQVTVAGSGSRPRSHHLHFSEV 2207
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2026 AA; 244061 MW; A0261E55A6F47A14 CRC64;
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BMBL; AB014849; AAN36432.1; -.

GO; GO:0004182; F:carboxypeptidase A activity; IEA.

GO; GO:0006118; F:electron transporter activity; IEA.

GO; GO:0006118; F:electron transport; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR000034; Cytc hame BS.

InterPro; IPR000034; Peptidase—MA.

PROSITE; PS00133; CARBOXYEPT ZN.2.

PROSITE; PS00190; CYTCCHROME_G; 1.
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Last annotation update)
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361 MPHKVHTCHISGLIHLE-
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Best Local Similarity 22.2.
Best Local Similarity 72.2.
Tocal Similarity 72.2.
                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
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NCBI_TaxID=36329;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
PRIO_0135.
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the human malaria parasite Plasmodium falciparum.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.4%; Score 160.5; DB 5; Length Best Local Similarity 19.6%; Pred. No. 0.066; Matches 70; Conservative 77; Mismatches 118; Indels
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Hypothetical protein.
SEQUENCE 2309 AA; 276528 MW; 8A6F8DBB972C4922 CRC64;
                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                    2309 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=3D7;
MEDLINE=22255705; PubMed=12368864;
                                                                                                                                                              Commercial (Trembirel, 23, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia, Colombia,
                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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01-MAR-2003
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MEDLINE=22255705; PubMed=12368864;
MEDLINE=22255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
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                Carlton J.M., Pain N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallon S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McRadden G.I., Cummirgs L.M., Subramanian G.M., Mungall C., Praser C.M., Barrell B.J., Hoffman S.L., Newbold C., Davis R.W., "Genome sequence of the human malaria parasite Plassmodium
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Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa; Haemosporida; Plasmodium.
VCB_TaxID=36329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDQNGFIVFQGDTPFLQCLNTVPTNM-----PHKVHTCHTSGLIHLERNER--IHL--KD 386
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Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S. Bertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B. Martin D.M.A., Fairlanb A.H., Fraunholz M.J., Roos D.S., Ralph S.A. McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Peter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.
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Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K.,
Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett of Commond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMEL/GenBank/DDBJ databases.
EMBL, AL644505; CAD50437.1; -.
InterPro; IPR000084; TSP1.
InterPro; IPR002035; WWF.A.
Pfam; PF00090; tsp_1; 1.
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Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM0027i; Dnaj; 1.
PROSTIE; PS50076; DNAJ 2; 1.
Hypothetical protein. 324824 MW; 9BDC29EE210E77B3 CRC64;
SEQUENCE 2738 AA; 324824 MW; 9BDC29EE210E77B3 CRC64;
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Nature 419:498-511(2002).
EMBL; AE014842; AAN36015.1; -.
INTERPRO; IPR001623; DnaJ N.
InterPro; IPR008941; TPR-Tike.
Pfam; PP00226; DnaJ; 1.
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                                                                                                                                                                                                                                                                                     63 RVSHLD-KELKSLKRVVDNL-------QQRLGINY---LDEFDEFQKEYEN--
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Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Last annotation update)
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SWART; SM00209; TSP1; 1.
SWART; SM00327; VWA; 1.
PROSITE; PS50092; TSP1; 1.
Hypochetical protein.
SEQUENCE 1371 AA; 160118 MW;
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SRSIADVRNEEQNIQGNHTELQEKSSNEATSKESPAPLHHRRAMHSRHRHLL 261	284 MSKIMDINENFLFSNQNEEMNISTHNTSNNVTPPLLNNNINMNDDLKNIY 333	262 VRKARSEDSRPAAHFHLSSRRRHQGSMGYHGDMYIGNDNERN 303	INSPYYDSSNN	SYQGHFQTRDGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQG 346	NVINIAGTKSSNTTSTNTFKFKKKYSSNFLKMFNKNIVKEYTSINTNNS 442	DIPFLOCINTVPTNMPHKVHTCHTSCLIHLERNERIHLKDIHNDRN 392	::	
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PFMAL7P1 07
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                   em_htg_hum: *
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                                                                          em htg mus: *
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-MODEL-frame+_p1.model -DEV=xlp
-MODEL-frame+_p1.model -DEV=xlp
-MODEL-frame+_p1.model -DEV=xlp
-MODEL-frame+_p1.model -DEV=xlp
-DE-CENT_frame+_p1.model -DEVEXLp
-DE-CENT_frame+_p1.model -DFVEX_FRAME
-DECALL_GROOT_DFVEX_FRAME
-UNITS=b1ts -CTART=1 -END=-1 -MATRIX=D108Um62 -TRANS=human40.cdi -LIST=45
-DOCALL_GRN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcc -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USRE-USO9813329 @CGN 1 1 7406 @runat 13092004 102753 21667 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADE1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                           September 15, 2004, 02:20:57; Search time 6712 Seconds (without alignments) 2641.135 Million cell updates/sec
                                                                                                                                                                                                   US-09-813-329-6
2162
1 MTAETLKPFITPTSANDDGF.....DRNAVLREGNNRSYFGIFKV 409
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                     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                          - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                             3470272 segs, 21671516995 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                 of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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                                                                                                          LeuGlnGlnArgLeuGly1leAsnTyrLeuAspGluPheAspGluPheGlnLysGluTyr
                                                        GACGATGGCGATGGTTCCATTGCGGACGACGACGACGACGACGTTAGCTATAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MTAETLKPPITPTSANDDGPPAKATSTATAQRKTRQLIPLVLGF
IGLGLVVALIALTIMQTTRVSHLDXELKSLKRVVDNLQQRLGINYLDEFDEFQKEYEN
ALIDYPKKVDGLTDEEDDDGDGLDSTANDEDDDVSYSSVDDVGADYEDYEDTNKLN
NAHTGTTPTSETTAEEGEGETDGASSASNDDNVFDDFTSYNAHKKKQERKSRSIADVRN
BEQNIQGNHTELQEKSSNEATSKESSPAPLHHRRRMHSRHRHLLVRKARSEDSRPAHF
HLSSRRRHQGSMGXHGDMYIGNDRRNSYQGHPQTRDGVLTVTNTGLYYVYAQICYNN
SHDQNGFIVPGGDTPFLQCLNTVPTNMPHKVHTGHTSGLIHLERNERIHLKDIHNDRN
AVLREGNNRSYPGIFFLY
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                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                            Igaki,T., Kanda,H., Yamamoto-Goto,Y., Kanuka,H., Kuranaga,E.,
Aigaki,T. and Miura,M.
Biger, a TNF superfamily ligand that triggers the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                      /gene="eiger"
427. .1656
427. .1656
/gene="eiger"
/codon_start=1
/evidence=experimental
/product="TNF superfamily ligand, Eiger"
/protein_id="BAC00950.1"
/db_xref="GI:21623742"
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Matches:
Conservative:
Mismatches:
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(bases 1 to 2101)

Inohara,N. and Nunez,G.

Direct Submission
Submitted (10-MAY-1999) Department of Pathology, Comprehensive Cancer Center, 1500 E. Medical Center Dr., Ann Arbor, MI 48109,
Location/Qualifiers
               Drosophila melanogaster tumor necrosis factor family member DTI (dt1) mRNA, complete cds.
AF149799
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ehydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2101)
Inohara,N. and Nunez,G.
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                                       ProAlaLysAlaThrSerThrAlaThrAlaGlnArgArgThrArgGlnLeuIleProLeu
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Submitted (15-NOV-2002) Berkeley Drosophila Genome Project, Lawrence Berkeley, CA 94720, USA Sequence submitted by:
Berkeley, CA 94720, USA Sequence Submitted by:
Lawrence Berkeley National Laboratory
Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence Enterley National Laboratory
Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence 2000. The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accuracity this particular cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAS, and reverse transcription of unspliced precursor RNAS, and reverse transcription about this sequence, including its location and relationship to other sequences, please visit our Web site cham@fruitfly.berkeley.edu) or send email to chamber the chamber of the principal province of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequenc
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ALID FEKVUGLTDE EDDD DEGOLDS STAD BEDDDOVSYSSOVDOVGAD VERDYTDMINKLN
NAHTOTTYSTTATA EGGEGETDS ASSAS NDDNVFDDFTS YNAHKKORRKSR SIAD VRD
EGONI OGNHTELOEKS SNEATSKERPAPLHHRRAMSRRRHLLVKKARSEDSR PADVRN
ELS SRRRHOGSMGYHOMY IGNDNERNS YGGHFOTROCHLYTNTGLY YVYKAICKNN
SHLONGFIVFOGD PERCHOLOCHLY VHTCHTSGLIHLERNER IHLKOLHNDRN
AVLREGNNRS YFGIFKV"
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MetThralaGluThrLeuLysProPheileThrProThrSerAlaAsnAspAspGlyPhe

. No.:

Met ProHisLysValHisThrCysHisThrSerGlyLeuIleHisLeuGluArgAsnGlu

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Drosophila melanogaster DARTH (darth) mRNA, complete cds.
  400
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Submitted (28-MAY-2002) Internal Medicine, UT Southwestern Medical
Center, 5223 Harry Hines Blvd., Dallas, TX 75390, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophiladae; Drosophilae;
Drosophiladae; Drosophila,
Kauppila,S., Maaty,W.S., Chen,P., Tomar,R.S., Eby,M.T., Chapo,J.,
Chew,S., Rathore,N., Zachariah,S., Sinha,S.K., Abrams,J.M. and
Chaudhary,P.M.
Eiger and its receptor, Wengen, comprise a TNF-like system in
                         ArgileHisLeuLysAspileHisAsnAspArgAsnAlaValLeuArgGluGlyAsnAsn
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1. 1248
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necrosis factor ligand family member"
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178. .1245
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Chaudhary, P.M.
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QICYNNSHDQNGFIVPQGDTPFLQCLNITVPTNMPHKVHTCHTSGLIHLERNERIHLKD
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bobtera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Bydroidea; Drosophilade; Drosophila.

(Bases 1 to 2159)

Moreno, E., Yan, M. and Basler, K.

Byolution of TNF signaling Mechanisms. JNK-Dependent Apoptosis

Curr. Biol. 12 (14), 1263-1268 (2002)

Change 1 to 2159.
                        TACATAGGAAATGATAACGAGAGAACTCTTATCAGGGACACTTTCAAACGCGCGATGGC
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Moreno, E., Yan, M. and Basler, K.
Direct Submission
Submitted (13-JUN-2002) Institut Molecular Biology, U
Winterthurerstrasse 190, Zurich, Z 8057, Switzerland
Location/Qualifiers
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All Direct Submission

Submitted (07-JUN-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
Berkeley, CA 94720
This clone was sequenced as cornary, presence of a polyA tail and contiguity
of sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptuse errors that result in single base changes.
For further information about this sequence, including its location
(http://fruitfly.berkeley.edu) or send email to
catalonship to other sequences, please visit our Web site
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Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
Pacel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
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/db_xref="FLYBASE: FR98303483"
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                                                                             AACACGGTGCCCACCACATAAGGTGCACACCTGCCACACGAGTGGTCTGATC
                                                                                                                                HisteuGluargasnGluarg1leHisteuLysasp1leHisasnaspargasnalaval
                                                                                                                                                                  Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                          mRNA linear full insert cDNA.
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Drosophila melanogaster SD18286 ful
AY119233
AY119233 4X119233.1 GI:21430829
FLI CONA.
Drosophila melanogaster (fruit fly)
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1. .1221
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AY119233
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AUTHORS
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SOURCE ORGANISM REFERENCE AUTHORS	JOHNAL AUTHORS AUTHORS	COMMENT	BOULCG	ORIGIN Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB: US-09-813-32 Qy 5
Qy 208	Qy 243	266	Qy 295 yrIleGlyAsnAspAsnGluArgAsnSerTyrGlnGlyHisPheGlnThrArgAspGlyv 315 Db 33775 ACATAGGAATGATAACGAGAAACTTTATCAGGGACACTTTAAACGCGGATGGCG Qy 315 alLeuThrValThrAsnThrGlyLeuTyrTyrValaGlnIleCysTyrAsnAsnS 335 Db 33835 TCTTGACGGTGACCATACGGCCTATATTACGTATACGCCCAGATATGCTACAACACT 33894 Qy 335 erHisAspGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeuGlnCysLeuA 355 Db 33895 CGCACGACCAGACGGATTTATCGTTTCAGGGAGACACTCCATTCTTCAGGCACTTCTTGA 33954 Qy 355 snThrValProThrAsnMetProHistYCTTCAGGGAGACCTCCATTCTTGA 33954 Qy 355 snThrValProThrAsnMetProHistYCTTCAGGAGACCTCCATTCTTGA 33955 ACACGGCCCACCAACATGCCCACACACCTCCCACACACGATGGTCTTGATCCTTCTTCTTCTTCTTCTTCTTTTTTTT	375 isLeuGluhrgdsnGluhrglleHisLeuLysAspIleHisAsnAspArgAsnAlavalL

100 TyrGluksrhlaleullaAspTyrProLysiysValhspGlyLeurhrapGl 117	The state of the s
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CTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTTGGGCATAAACTATCTGGACGAGTTC 136457
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                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuAlaLeuThrIleTrpGlnThrThrArgValSerHisLeuAspLysGluLeuLysSer
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                                                              /clone="BACR06001 (D601)"
/clone lib="RPCT-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
pBACe3.6)"
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Matches:
Conservative:
Mismatches:
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      /db xref="taxon:7227"
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/map="46C-46D"
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Drosophila melanogaster

Bukaryota; Metazoa, Arthropoda; Haxapoda; Insecta; Pterygota;

Bukaryota; Metazoa, Arthropoda; Haxapoda; Insecta; Pterygota;

Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Celniker, S.E., Adams, M.D., Krommiller, B., Tyler, D., Wan, K.H.,

Holt, R.A., Evans, C.A., Gocayre, J.D., Amanatides, P.G., Brandon, R.C.,

Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,

Carlson, J.W., Center, A., Champe, D., Doyle, C., Dresnek, D., Eraser, S. Frise, E. Galle, R.F., Garg, N.S., George, R.A.,

Gonzalez, M., Houck, J.J., Hoskins, R.A., Hossin, D., Howland, T.J.,

Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,

McIntosh, T. C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,

Pacleb, J., Paragas, V., Park, S., Patel, S., Patel, Er, P.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Sequencing of Drosophila chromosome 2R, region 46C-46D

Unpublished

El (Bases 1 to 172904)
                                                                                                                                                                                     This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
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Submitted (28-APR-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Sep 6, 2001 this sequence version replaced gi:13324748.
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BAC clone
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                                                                   BnThrValProThrAsnMetProHisLysValHisThrCysHisThrSerGlyLeuIleH
                                                                                                                                                                                                                                                                                                                                                                     172904 bp DNA linear INV or DAGROUPILA melanogaster, chromosome 2R, region 46C-46D, BACR06J01, complete sequence.
                                                                                                                                                                                                                                             Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
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/strain="y; cn bw sp"
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Qy 266 ArgSerGluAspSerArgProAlaAlaHisPheHisLeuSerSerArgA 282 Db 138256 TTCTTTCAGCCGAATCCGAGGCCAGCAGCCATTTCCACTTGAGCAGCAGCC 138315 Qy 282 rgArgHisGlnGly	RESULT 10 AC099029/C LOCUS LOCUS DEFINITION Drosophila melanogaster chromosome 2R, region 46D-47A, BAC clone ACCESSION VERSION AC099029 GI:16798961 VERSION AC099029 GI:16798961 REPRINCE Drosophila melanogaster (fruit fly) HTG. BUATOOTA: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Brosophila melanogaster Coropolaterygota; Dipters; Brachycera; Muscomorpha; Brydroidea; Drosophilade; Drosophilade; REPERBING ENATIONS ROSOPES: E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., HOL, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R. Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., ROGES, Y., An, H., Baldwin, D., Bancon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Carlson, J.W., Center, M., Champe, M., Davenport, L.B., Dietz, S.M., Carlson, J.W., Carler, M., Galle, R.F., Garg, N.S., George, R.A., Ibogwam, C., Jalali, M., Kruse, D., Li, P., Matter, B., Roders, J., Smith, H.O., Rubin, G.M. and Venter, J.C., Staplecton, M., Strong, R., Svirskas, R., Petelfer, B., Pholuanenavong, S., Pittan, G.S., Puri, V., Richards, S., Scheeler, F., Saveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Callson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Callson, J.W., Center, A., Gocayne, J.D., Amanatides, P.G., Brandon, R. Sequencing of Drosophila chromosome 2R, region 46D-47A HORDISHERNER C. Chamses I to 189620) AUTHORS AUTH
137118 TCGCTTTTGGCTGTATGTGACGATTGATCGAATCTCATCAAATGCCCTAATGCCCAGAGA 137177	UGIYGIUThiraspSeralaSerSeralaSeraenaspAspAspAsivalPheaspAspPheTh GGGCGAGAGCGACAGTCCTCCAGCCTCAAATGACGACTGTTCGATGGTTCGATGACTTTAC FSETYRAShAlaHiSLYSLYSLYSGLOGCACAAATGACGATGACATGTTCGATGACTTTAC FSETYRAShAlaHiSLYSLYSLYSGLOGAAATGATGACAATGTTCGATGACTTTAC FACTACAATGCCCACAAAAGAAGAAGACAGGAAATGATGACAGGATGAATTTCAGGGA TTTATCGTATTAAGCCTCTGCTTTTCCTCTTCACAGAAATCTCGCTCG

us-09-813-329-6.rge

Gonzalez,M., Houck,J., Hoski Ibegwam,C., Jalali,M., Kruse, McIntosh,T.C., Moy.M Murbh	Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIntosh,T.C., Mov.M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo.J.,	<u>ک</u> ط	99 99 165980 CCTGTTTTTGAAAAAGAATGCCTGAAAAATGACCAGACGTAATATGTGGTTATTGTGT 168921
Pacleb,J., Paragas,V., Park, Phouanenavong,S., Pittman,G.	 Patel, S., Pfeiffer, B., Puri, V., Richards, S., Scheeler, F., 	ò	
	rskas,R., Tector,C., Williams,S.M., in,G.M. and Venter,J.C.	qa	165920 GGGACATACAAAATATTATAGAATTATGTGCTAAAATATAATTTCGACGCTGTTTCAT 165861
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166100	TATATCGAACTTTTGTTATTGAGTATCTATTATGTTTTGTTTTTTTT	qq	
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Reoptera; Endoperygota, Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (Dasse 1 to 275390) Adams, M.D. Celliker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Ammartides, P.G., Scherer, S.E., Li, P. M., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Li, P. M., Abbriner, M., Henderson, S. M., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X., Baradon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Hell, G., Nelson, C.R., Gaborr, G.L., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Baxendale, J., Bayraktaroglu, L., Bolshakov, S., Benson, K.Y., Benso, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Burtis, K.C., Busam, D.A., Butler, H., Cadleu, E., Center, A., Cahles, P., Chandra, J., Cherry, J.M., Cawley, S., Dahlke, C., Davengort, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Ferrier, S., Pleischmann, W. F., Dunnes, M., Dugan-Rocha, S., Pleischmann, W. F., Daviel, S., Pleischmann, M. F., Bandaris, T.C., Ferras, C., Ferrier, C., Ferrier, C., Ferrier, C., Ferrier, S., Pleischmann, W. Forler, C., Cabris, J. P., Cahris, J. P., Carris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahrange, J., Cahris, J. P., Cahris, J. P., Cahris, J. P., Cahris, J	Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Guan, P., Harris, M., Harris, N.L., Harvey, D., Hehman, T.J., Herrandez, J.R., Houston, K.A., Hehman, T.J., Herrandez, J.R., Howland, T.J., Herrandez, J.R., Howland, T.J., Merin, M.M., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kannison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X., Mattei, B., McIntosh, T.C., McLeod, M.P., McDherson, D., Merkulov, G., Mishina, N.V., Mobarry, C., Muzskern, D.B., Nolson, D.L., Nelson, D.R., Mount, S.M., Moy, M., Murphy, B., Murphy, D.M., Nelson, D.L., Nelson, D.R., Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puri, V., Reese, M.G., Fanner, K., Remington, K., Sumpson, M., Stroeler, F., Shen, H., Shue, B.C., Sjradling, A.C., Sumpson, M., Stroeler, F., Shen, H., Shue, B.C., Sjradling, A.C., Stapleton, M., Strong, R., Sun, E., Svirskas, R., Tector, C., Turner, R., Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodeg, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, R.F., Sheng, K., Morley, K.C., Wu, D., Yang, S., Zhu, X., Smith, H.O., Scheng, T., Globs, R.A., Myers, E.M., Rubin, G.M. and Venter, J.C., Tonony, W., Zhong, W., Zhou, S., Zhu, X., Smith, H.O., Tonony, W., Zhong, W., Zhou, S., Zhu, X., Smith, H.O., Science 287 (5461), 2185-2195 (2000) Celliker, S.E., Adams, M.D., Kronmiller, B., Wan, K.H., Holt, R.A., Baracon, J., An, H., Baldwin, D., Manatides, P.G., Berandon, K.C., Rogers, Y., Ranson, J., An, H., Baldwin, D., Manataldes, P.G., Berandon, K.C., Rogers, Y., Ranson, J., An, H., Baldwin, D., Manataldes, P.G., Berandon, K.C., Rogers, Y., Rogers, M., Rogers, M., Chang, M., Chang, W., Zhong, P., Shangon, J. W., Center, A., Change, M., Davengort, L., Baldwin, D., Paragon, J., Balazon, J. W., Shangon, J. W., Center, A., Change, M., Davengort, L., Baldwin, D., Shanzon, J., Balazon, J. W., Shanzon, J., Buller, M., Shanzon, J., Balazon, J. W., Shanzon, J., Balazon,	Perriera, S., Frise, E., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Houck, J., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., Moshrefi, B., Moshrefi, B., Moshrefi, B., Moshrefi, B., Moshrefi, B., Moshrefi, B., Moshrefi, B., Moshrefi, B., Moshrefi, B., Moshrefi, B., Moshrefi, B., Moshrefi, B., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phousnenavong, S., Pitthan, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D., Williams, S.M., Zaveri, J.S., Smith, H.O., Vencer, J.C. and Rubin, G.M. Sequencing of Drosophila melanogaster genome Unpublished 1 (Jases 1 to 275390) S Misra, S., Crosby, M.A., Matthews, B.B., Bayraktaroglu, L., Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W., Campbell, K., Hradecky, P., Huang, Y., Kaminker, J.S., Prochnik, S.E., Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W., Grey, A.D.N.J., Hardecky, P., Musso, S., Searle, S.M.J., Smith, E., Smuthiak, F., Whitfield, S.J., Ashburner, M., Gelbart, W.M., Rubin, G.M., Mungall, G.J., And Lewis, S.E., Annotation of Drosophila melanogaster genome Unpublished 1 (bases 1 to 275390)
REFERENCE AUTHORS	TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE
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Direct Submission
Submitted (33-JAN-2003) University of California Berkeley, 539 Life
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On Jul 1, 2002 this sequence version replaced gi:10727672.
Location/Qualifiers
                                                                                                                                                                                                                                     Direct Submission
Submitted (06-SEP-2002) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
6 (bases 1 to 275390)
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REFLDHGKRALAVSARSINELKLWNIKTNTCLQSLDEHUDRVWALAVSARSINRFFYTGGA
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ALLDPKARFYYNGNMVEVLTPYVQRHFKRVTELNKDLAFLEFIVKCM"
                   Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Direct Submission Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA (bases 1 to 275390)
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CONSRTM
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	234951 TAAACTCAACAATGCACATGACCGGCACCACATCTGAGACCACTGAGGGCGA 235010	177 uGlyGluThrAspSerAlaSerSerAlaSerAsnAspAspAsnValPheAspAspPheTh 197	235011	197 rSerTyrAsnAlaHisLysLysLysGlnGlu	235071	208	235130 TTTATCGTATTAAGCCTCTGCTTTTCCTCTTCACAGAAATCTCGCTCG	216 lArgAsnGluGluGlnAsn1leGlnGlyAsnHisThrGluLeuGlnGluLySSerSerAs 236	235190 ACGCAATGAGGGGGGGGATATTCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAA 235249	236 nGluAlaThrSerIysGlu242		242 242	0	243	235370 TATGTATACATTTTCTTTTACTTGAAGCCCTGCACCACCACCGTCGCAGGAATGC 235429	254 isSerArgHisArgHisLeuLeuValArgLysAla		265 265	235489 ITGGCAAAAATGGAATACCAAATCTCTATTCGCACCTCTGTTAATTTGCAGGTGAATCTC 235548	266ArgSerGluAspSerArgProAlaAlaHisPheHisLeuSerSerArgA 282		282		287	ACTACAGGCAACCTAATGAAGTCACTTCTTGAATTTCTCA-GGCTACCATGGAGATATGT 23	295 VIIIeGJyAsnAspAsnGluArgAsnSerTyrGlnGlyHisPheGlnThrArgAspGlyv 315 	315 alleuThrValThrAsnThrGlyLeuTvrTvrValTvrAlaGln1eCvsTvrasnAsnS 335		335 erHisAspGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeuGlnCysLeuA 355	55646 CGCACGACCAGAALIIAICGICIIICAAGGAGACACICCATICCIGCAGIGCITGA	355 snThrValProThrAsnMetProHisLysValHisThrCysHisThrSerGlyLeulleH 375 	375 isLeuGluArgAsnGluArgIleHisLeuLysAsDIleHisAsnAspArgAsnAlaValL 395 235968 ACTGGAACGASACGASTASTASTASTASTASTASTASTASTASTASTASTASTA	395
66	, 0	VQ 99		6	IGCG	VQ 86			FCAT 234170	:	GTG 234230	VO 66	234290	λδ 66	Db Db Db Db	ζΩ 66	CGA 234410	VQ 66		VQ 66	ATT 234530		ACG 234590 Db		234650	99 (Q)	234710 Qy	Db	0y 0y 0y 0y	IGA 234830	OV 137 OY Db Db Db Db Db Db Db D	Qy Qy	234950 Oy
- 66	233871 TITACAAAGTCGGAAATGATTGTTATTCCTTGAGGCTGGTACTTGAGTTTTTAATGAGGG		233931 TATATCGAACTTTTGTTATTGAGTATCTATTATGTTTTAGTTTTCTTTTTGCCTAAAGGGT	66	233991 AATTIGCATTITATGAIGGCAAACTCIGGCTAGGGIATCICACAGGIGGIAAGCCA	66	234051 CCTGTTTTTGAAAAAGAATGCCTCAAAAAATGACCAGACGTAATATGTGGTTATTGTGT		234111 GGGACATACAAAATATTTATAGAATTATGTGCTAAAATATAAATTTCGACGCTGTT	66	234171 CTGTTATTTGTTTCATTTTTTTTTTTTAGCTGCTTGGCCAAAGGCACATAGAAATT	66	234231 ATAGATTATTGAATTATAATGTCTCTTTCCGCAAGGAAACACTCATTTCAAATATGAGG	66	234291 CGCCAGCCAGTTCACGTAATTTATGAGATACAAATCCCCAAGTGACAAAAGGTAAAAGCC	66	234351 CCAATAATTCAACAAAATACTAGGCTCTATCAGTAGATATAGTCGTTCAAGGCGAG	66	234411 TCGCTTTTGGCTGTATGTGACGATTGATCGAATCTCATCAAATGGCCTAATGGCCAGAGA	66	234471 TGGTTTTAAGATTTTAAGATTTATTTATTTTGATGGCTGGGCATCTGTGGTGCCA		234531 CTCTTGAGAGTTTCCTTCGCTTTTAAATATATGTATGATGTACACAAGTATATGTAT	66	234591 AGTATCATGTTTTTGAGCGAGGCGCCATCAATTAGGATGATGACGAAACAGCCTGTGCTG		234851	234711 CAGCTGCAGTCACGTACTTGGCCAAGTCTTCTGACCCAAATGGTGATGCCCATCCC		234771 GITGCAGTACGAGAATGCCCTCATCGACTATCCAAAAAAGGTGGATGGC	117 uGluhspaspaspdspglyaspglyLeuaspSerIlealaaspaspGluaspaspass 11		234891 TAGCTATAGCTCTGTGGATGATGTTGGCGCAGACTACGAGGACTACACGCGATÀTGTTÀAÀ. 157 nLysLeuAsnAsnAlaHisThrGlyThrThrProThrSerGluThrThrAlaGluGlyGl
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                                                    CDS
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L. Nature 419 (6906), 527-531 (2002)
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                                                                                                                                                                                      INV 29-JAN-2003
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

I (bases 1 to 188548)

Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T.,

Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T.,

Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S.,

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Moule, S., Murphy, L., Oliver, K., Quail, M.A.,

Rajandream, M.-A., Rutter, S., Skelton, J., Squares, S.,

Sulston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and
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AL014558 AL008982 AL008989 AL009007 AL009008 AL009009 AL009014
AL010110150 AL010152 AL010156 AL010158 AL010211 AL022217
AL034558.3 GI:15375364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete nucleotide sequence of chromosome 3 of Plasmodium
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                                                                                                                                                                                      DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 400 (6744), 532-538 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'mol type="genomic DNA"
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                                                                                                                                                                                      158548 bp
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PFMAL3P2
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donor Tor exon /
4 weak Pfeam matches to entry PF00023 ank, Ank repeat; Pfam match to entry PF01529 zf-DHHC, DHHC zinc finger domain, score 66.70, E-value 4.8e-16
Similar to Plasmodium vivax pv1114090 pv1114090W
SWALL:AAF99464 (EMBL:AY003872) (611 aa) fasta scores: E():
5.6e-172, 71-94* id in 613 aa, and to Mus musculus
503446114rik protein 5033406114rik SWALL:Q9D3Q8
(EMBL:AK017158) (368 aa) fasta scores: E(): 1.7e-09,
24.87* id in 197 aa, and to Rattus norvegicus small rec
srcc SWALL:Q9JKRS (EMBL:AF228917) (366 aa) fasta scores:
E(): 8.4e-09, 27.95* id in 161 aa"
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/codon start=1
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/product="binding protein, putative"
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YYSSIENKNYNYGOCIKNRYFULLINTUTNYFRENGURNYK
NIQSSKYKNSNPMYNGTFKTNAEYOLNNIEREIFOINKKLISTNFNTTPINHDQALS
NKYNDILNIERSYGKSLSLYSGVSERINSCHENGURNYCYTLIFPRYNT
HICKECFHCIVHQDDHICWWDNCIGIKNQRCFYMFFFCIFVLLLYNYYYYVLYFHERO
ATINYAFGSLVILCNFINYTHAESHITYLFARNIFTILINUTFYEHYKRPNITIDKYNT
#341 1001
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PPPKYKLI I HPTLLNVNEQNNSNI EI AREILYLGIYI RKI QKPI EI NKRSQSCNPTPD
I FCCCLSNI SAHILNHI NRI EENVRNI YNFTKI NMKHNSTNNYNNNNNNNHDNNNPI
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NKYENNDFWKYENIYGNDNIIKRSVQEEEEKKKWIEDNYNKESSLEFTYPYRYBENRN
IFLIINSENINLGNSCYYNNDLIYIIHNNKRYEHMNLPKRTKKKKKKKKKRTKETKRK
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LLKNITTPLFDFIKNYIFYGKVKDTYKEPFIHENKHITPYYKQNHKPYFNNMYKYIPK
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LIDQNEYKNI NENI DI NMDTNQNNRNS PLFPKDVI YKR I YNENI NNDQYTNSDHI RNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similar to Plasmodium vivax pvlh14095 p pvlh14095W SWALL:Q962L5 (EMBL:AY003872) blast scores: E(): 0.0, score: 2249 43% id, and to Plasmodium falciparum thloredoxin-like redox-active protein freb SWALL:Q9NC62 (EMBL:AP23463) (179 aa) fasta scores: E(): 7.5e-47, 99.42% id in 175 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5341. .12021
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/note="Revised: original entry split into PFC0165w and
                                                                                                                 /note="Revised: revised to 8 exon structure, revised:
join(1030. .2337,2429. .2502,2645. .2685,2826. .2941,
3046. .3173,3308. .3388,3508. .3571,3699. .3737)
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protein jd="Chass989.3"
/db_xref="G1:23477022"
/db_xref="GPTREMBL:097225"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonym: PFC0165w"
                                                                              /gene="MAL3P2.1"
                                                                                                                                                        donor for exon 7
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/gene="PFCO166w"
/note="synonym: frep"
12790. .1329
/gene="PFCO166w"
/note="Revised: split original spliced gene PFCO165w into PFCO165w and PFCO166w, fasts.; Plasmodium falciparum; thioredoxin-like recovactive protein; frep; length 179 as; id=100%; ungapped id=100%; E()=2.1e-69; 179 aa overlap; query 1-179 as; bubject 1-179 as; fasts; PN-14100 p; pv1h14100W; length 179 as; id=65.92%; ungapped id=67.42%; E()=1.5e-46; 179 aa overlap; query 1-177 as; subject 1-177 as averlap; query
                                                                       NENYHDOQVANNSETIEDENENYHDOTATIETENYMONDITELENYMONDITENYNN

NENYHDOQVANNSETIENEN SURWENNYNNANNANNANNYNNYDDMSGNPLLKNIKN

NNFILKNITKKKONYSKI.NELRRNKKTNNMMNTNNNNNNNNNNNDDMSGNPLLKNIK

NNFILKNITHNNNYPSNNANTEN YKKKTNIKNTTHRYTNITHTTHKYTTLIFRYLNYCK

Y IEHKLASEVMLANHPYKNIN IN RECTRINLAT CIHTRECHI HELKCYLYHIQUDVIKSE

YKNNMNTKLKETLIFDDI IHIHNTYLNNILKYSFIMDNI ITCLIKLISISHIFRRHIL

KENPEKREQIENTITHHAVKSNYLNPNTHINNHPHNQYTNNNKNNNNNNHKKIIQE

LLLASYQNPTSFNNDI INSEYVNDRFNDNLDDSNUTRQVTKENNNCTNYNNNUSKYNNHMC

SNNPIESNSVQIKRKKNILLMNDRNYNNI DENNHTNINDMNNINNNNNNNNNNHRN
                YLEKLYHYKKNNILNXLKNFFDISIRSSVLYHLKYKKDYNVAISDIFSIMDNVNLIID
LRKFQISNEQQGLNKKGANNYEEVHDGDDDDDYYNNNGNEYNNYEEGYNDDEBERNNY
                                                       LNKNDYDDEQEADDEEEDDDDDDDDYDNDDDDEYKEYENDNGNDNYDEADSDHNNYNNT
                                                                                                                                                                                                                                                                             ITSEIKNHSPNEYRNNIITNHTINNNCNSNYHQINYSLHRFSNNNNNNNNNKYQSEL
HNLNDKSNFNKKDNYNINDTNNNNYHYTNNNTSPKSSNEKNKIYNNHPINYMRNDYNK
NILNNNKOTILSENPYLKEKNHIPFONKNHDTPSPLHINNFNQDENNNISPLNYSKLK
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YFKDKYLGLFFGASWCKYCVTFIDSLNIFKKNFPNVEIIYIPFDRTYOEYGSFLKNTN
FYALPFDNYLYICKKYQIKNLPSFMLITPNNNILVKDAAQLIKTDEYINNLKSLIKNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140.90, E-value 2.2e-38; Pfam match to entry PF00364 biotin_lipoyl Biotin-requiring enzyme, score 46.20, E-value 7.4e1.0 Similar to Arabidopsis thaliana branched chain alpha-keto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Similarity to lipoamide acyltransferases. eg
C.elegans lipoamide acyltransferase (WP:ZK669.4) BLAST
Score: 582, sum P(1) = 9.2e-57, 33% identity in 430 aa
overlap; similarity to P. vivax PVH14105C, 59.90%
identity (61.611% ungapped) in 434 aa overlap
Ffam match to entry PP00198 2-oxoacid dh, 2-oxo acid
dehydrogenases acyltransferase (catalytic domain), score
140.90, E-value 2.2e-38; Pfam match to entry PP00364
                                                                                                                                                                                                                                                                                                                                               KFNTSYNNNENIKNINLSNIDLDSIDNSRYSSKYNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GOA:Q81224"
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/gene="MAL3P2.3"
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                                                                                                                                                                                                                                                                                                                                                                  gene
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158548
                  82
57
150
85
       Length:
Matches:
Conservative:
Mismatches:
Indels:
        0.433
175.50
37.17%
21.93%
8.12%
                                 Best Local Similarity:
                        Percent Similarity:
Alignment Scores:
                                         Query Match:
DB:
          ..
No..
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US-09-813-329-6 (1-409) x PFMAL3P2 (1-158548)

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LysGluLeuLysSerLeuLysArgValValAspAsnLeuGlnGlnArgLeuGly1leAsn 88 69

6174 6231 6291 6396 6456 6510 5902 AATCAAGATTATCATGATAAAGACGATGATGATTATGATGATGATGATGATGATGATGAGAT 5961 143 163 ThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluThrAspSerAla 183 302 CACAATGTGAATAATATAAAT---AATTATAACATGCGCGAACATTTAAAAGGATAGAA 6747 321 ThrGlyLeuTyrTyrVal-----TyrAlaGlnIle-----CysTyrAsnAsnSer 335 HisThrSerGlyLeuIleHisLeuGluArgAsnGluArgIleHisLeuLysAspIleHis 388 144 AspValGlyAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHis -----GACACATTTGGTTCTGTTACTAGTATGAACGATGAAAAGGATTATATGAAATAT 104 LeulleAspTyrProLysLysValAspGlyLeuThrAspGluGluAspAspAspAspGly SerSerAlaSerAsnAspAspAsnValPheAspAspPheThrSerTyrAsnAlaHisLys 124 AspGlyLeuAspSerIleAlaAspAspGluAspAspAspAspValSerTyrSerSerValAsp ---LysSerSerAsnGluAlaThrSerLysGluSerProAlaProLeuHisHisArgArg 252 ArgMetHisSerArgHisArgHisLeuLeuValArgLysAlaArgSerGluAspSerArg 3346 GAACAATTTATAAATTATGATGATGTTATTTTTAGAAAATTTCAAA--------6631 AATGTTGCCTCACATATAAATAACAACAAATAATAATATGAACAATATAA 272 ProAlaAlaHisPheHisLeuSerSerArgArgArgHisGlnGlySerMetGlyTyrHis 292 GlyAspMetTyrIleGlyAsnAspAsnGluArg-----5457 CTTATTAATGAATATAACACGGTCACAAAAAATGAT-----TTAGTAGATATAAAT ------GlnCysLeuAsnThrValProThrAsnMetProHisLysValHisThrCys 219 -----GluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGlu-----------AsnSerTyrGlnGlyHisPheGlnThrArgAspGlyValLeuThrValThrAsn LystysGlnGluArgLysSerArgSerIleAlaAspValArgAsn-----HisAspGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeu----6748 AAAAAAAAAATAAATAATAATTATAATAATAATAAT 6789 389 AsnAspArgAsnAlaValLeuArgGluGlyAsnAsnArgSer 402 TyrLeuAspGluPheAspGluPhe 369 352 6691 S S δ 임 ò g

RESULT 13

	RESULT 14 PEAS29352 ILCCUS PEAS29352 PEAS29352 PEAS29352 PEAS29352 PEAS29352 PEAS29352 PERSZERIC 14 PERSZERIC 15:2504570 MISSERIC 16:2550470 MISSERIC 16:2550470 MISSERIC 16:2550470 REFERENCE 16:2550470 REFERENCE 16:250470 REFE	D
PFMALIP2 2 WPCOMMENT Sequence split into 4 fragments LOCUS PFMALIP2 Accession AL031745 Sequence split into 4 fragments LOCUS PFMALIP2 Accession AL031745 PFMALIP2 1 100001 100000 PFMALIP2 2 200001 310000 PFMALIP2 3 300001 310000 PFMALIP2 3 300001 310000 PFMALIP2 1 100001 310000 PFMALIP2 2 100001 310000 PFMALIP2 3 300001 310000 PFMALIP2 3 300001 310000 PFMALIP2 3 300001 310000 PFMALIP2 2 100001 310000 PFMALIP2 2 100001 310000 PFMALIP2 2 100001 310000 PFMALIP2 2 100001 310000 PFMALIP2 2 100001 310000 PFMALIP2 2 100001 310000 PFMALIP2 2 100001 310000 PFMALIP2 2 100001 310000 PFMALIP2 2 1000000 PFMALIP2 2 1000000 PFMALIP2 2 10000000000000000000000000000000000	Db 72719 AAATTGGATAGGTAAATTGGATAAATTAAGGATAAAATTATAGGATAAAATTATAGGATAAAATTATAAGATAAAATTATAAATTAAGATATAAAATTATAAATTAAGATATAAAATTAAGAATTAAAATTAAAATTAAAATTAAAATTAAAATTAAAATTAAAA	308 HisPheGinThrargaspGlyValleuthrValthrashThrGlyLeuTyrTyr

gene

CDS

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SKNKKONKGSDASFSSSDDTDDKLSSNKSELNYEENGHKKONKLLLEVHHDEIDYIPI
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PNYIONMAKLLLYFIIIVROKOPHIEDYIHRIGEGSIYNILANCKROVGTANISATP
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LANNIYYLLNYTIDIPOLEBMIIEDYIHRIGFRGRANNIGYAFTLLPREYTKANDIYNI
I NNNMNNDEEDD I KERKNLGLMSSDDEGDSHSDSHSDSHSDSNSDSNSDSNSDS
HSDSNSNSHSDYSYKKKKHSHHHSKYKKKHSHHRSKNKKKHSHHHSKKEKH I SNDTHK
SDEKHRKY I SSKKKK I KKEEKKKKKNYHSKKMKY I TYSNSSD"
                                                                                                                                                                                                                                                                                       /note="similar to Rattus norvegicus RNA helicase TR:Q62780 (EMBL:U25746) (1032 aa) fasta scores: E(): 2.4e-59, 38.387% id in 719 aa" /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /procedn id="CAD51452.1"
/procedn id="CAD51452.1"
/db_xref="GOA:021453"
/db_xref="GOA:021416"
/db_xref="SPTERMEL:081416"
/db_xref="SPTERMEL:081416"
/db_xref="SPTERMEL:081416"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YPSYAYKKKSSYHHVHREKYPDEKRKKYYEHICKKNKRRSYDYSSNYDESDFSSTSSY
YNERNKKYYKYEDKKKKEKEKEKEKERKRKKRYHHTDDDQDHLESYSSSRSSSRSSIN
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THYESDEETRUDESUNNUNNUNNUNNUNNUNNUNNUNNUNSESSELIAKTHEQEKES IN INKTSKEN
QEICEENKKEI OKVERMSNVKYTTENNUN SSEBLIAKTHEQEKES IN INKTSKEN
LATKVNKI KALNI FINDQDDESDNSKEKEFDI KNENKI INVQNVDDNNHKDDTKKKI YE
NHKI KEBSUNTNDI HAVDE INNKNEDALDLEMKEI EQACEEREKAVKKES ITLDEI TYTYD
MNKOKYE PFI NPKNHEI KEYNKKKI AKKKKINI OQGNI HEKQDSSNVHTGEDLKKENKNI TK
NTTNNNY SDNNNNUDDDDDDDDDDDVVHKLEYEELKKKTEEDMKRNEKONNI TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKWNDTWELSLKAKKINELMKTYNFLSLQENHDKFLKNAQYEBFDKIAEKEALKVTËH
TKDEKKKLI-IPKTKALIQKIKAGOPUNESIQRNMLSALRTKMKKYSBYLD
HTYITEDNNI LEBEYINYPQHVRLKI SHKOVLAKIADMSGATCQI KGQYSNESGPNK
ONFLLDTKQLHIEILAPITYNQIQIARNELNSLLINNFMISCNI KAKRASTGWAPP"
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GDKVATFSLATNE FWRDRNTNELKSKTDWHRIVVYDQNIVDLIDKYLRKGRRVYVQGS
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EHINNNNINNGNDFMPLNSNDKIIEDKEFTDRLDDNNEENNFQSNSETFDKQEIYDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="single-strand binding protein, putative"
/protein_id="CAD51453.1"
/db_xref="GI:23504574"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="ATP-dependent RNA helicase, putative"
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                                                                                                                                                                                                                                    gene="PFE0430w"
                                                                                                                                                        /gene="PFE0430w"
11261. .15733
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/gene="PFE0440w"
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/gene="PFE0440w"
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LFEKSROYCNI VSVPTKVILHNNI YI KDILAGNTYS I ILSVDGFI YI FGGFI KGSNGN
SNNGSCRYISLYNBI THVYKYMNGKY BHYFLFTYDNKLFGIGNNKNCOLLCDNEKENNY
IKRPKLI TYFLKENNKI I ESI FSFHNYFI OFNNS EI PRAGYTNNYHLCI GI PNNI KY
LKHPKTI KTWLYPOKOLDYNGSCSDMBLNEYNTTNNMSYNNYI KYINEI TLUKKNI
NYTELFONEYTYRGY YEBEI BRRI YNI VIMNNI INWCHLQNLLKKEEYNNNMSY I KSF
BKDI JOLYSKHI BYLLANINI YEKQFIYLLINOYDS FLLSHI AMKREQHLINILYPFSTY
I FDQNR I KLEOFI YI I QQQPYLL I LCLI HNYROWRAYKQLMYGKASYNSNRATTHIY
HNNINEQHI KNNYNI INSNY INHTYNY EQNDALKKYNSKO JQNKKYS FYRNSSNACK
FI FDLYADPRIRRWRYTI FI FILIKLGI EI KKSILNYHSI FNI DTSI FFKK
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YVGFFNITNDYNYYISKLGHANDDIDIYYPKLOEATHASTYVCTGGTTLVDDIJSGCRNSLANKNY
SYEKEINDNIDSDDDILXYLINKEVERECHYNGDNKSYLDHASTYVCTGGTTLVDDILSFGNYKNY
YVERREINDNIDSDDDILXYLINKEVERECHYNGDNKSYLDHASTYVCTGGTTLVDDILSFGNYKNY
HYIKEMRGKMYIKDIVTHFYNLDTMTYYMNKINKHINGHYNNNDNYYTYDNINGSHG
NIERKNKLIKKSKVKIIDGSDHFSVFLLESGKYYTAGYNKNGBENLKKKFGVP
ILLANICVNKTIKRAGSTNYVLVCSDVGLYVGNGKNDKSQLGIGVIKDPYEPVHYKNLT
NVINIFAGYDHSACIINKLLDKGNYNVVNNVNNVNNVNNYSOSDCGCLLYNGNAE
NVINIFAGYDHSACIINKLLDKGNTNOVNNVNNVNNVNGVNGVNNYSSDECGDLYTWGNAE
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TPIFLEPHSVDNNGDNNDDYDDDNNNNSTYKPHKKEDSIKWDKKKNVVIHCSAGSKH
SLACNLHGDIYSWGYGGNGRLGLGNIKSYNKPQLIKGLRNKRILYVCAGTSHSGCIDS
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IVNDHTNEDRQSDINETIDKHSNDNDYDDEKKKEKMNIYKNKEKLYSNIKENDNKHDW
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FHYHLINRNSYYVQLKLFQVCHIFNLFFRFQNYLMLSFNDFALDIVNFFYTXKNNIPIQ
KHKHKHTLNSTMVGTNKMDIQKERERHINIKGLGKDMGNIQRPKGVSTFGTHQDNKKI
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AFNLPSTIKITSNDNKMRKKMKRLIFSEDDIEFFIKCKLIYNVKLDIRFLLKEKNMSI
CEFTKIPMPQYICYRKQTLIENNBYLFSIIHKYNYEKNNIYIISECLKNCPILEHCTD
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/translation="MPSKSGRVRMPADNRLPVSASLKTSEIWKNSVGYDPYASYEEIN
KKKEKKDEDINEKAKNLFNLSRLTGITSTTIPGACTVCNHIGHLPYQCRNFISLEKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MYEQDDEDKDIHKYIFPFFPKISTGLDHYACVAYYKNKPSIFTW"
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QNENLDNNDNYVEINFVCIFEELCKIFLNIKFPDMFKIIIKELFKYFIIYEKNLNDEI
NQTNKIYFYQNHHTIYIPFFKLILMAIINPILKNMENIAHKFSYPNIFPHILNIRNKI
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IKFSLILTKDQNKNIINEHTFTGSEIYSMYNSSPYILYPFFKYSKTYLCSITGLHFMH
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                                                                                                                                                                                                                                        aa) fasta scores:
                                                                                                                                                                                                                                                                                                                                                           'product="guanidine nucleotide exchange factor, putative"
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protein f8n16.20 TR:Q92V23 (EMBL:AC005727) (332 aa) fasta
scores: E(): 2e-12, 28.763% id in 299 aa" (5000 starta)
                                                                                                                                                                                              guanidine
                                                                                                                                                                                      /note="Similar to Plasmodium falciparum nucleotide exchange factor pfrccl (1327 E(): 9.6e-190, 97.459% id in 1338 aa"
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protein id="CAD51451.1"
db_xref="G1:23504572"
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/db_xref="GI:23504571"
                /gene="PFE0420c"
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/gene="PFE0425w"
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/gene="PFE0425w"
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Jia, Y. and Cherry, J.M.
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Dietrich, F.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164899 TATAAGAATAACGAAATATATGATAAAGAAAATATCGTAGAAATCAAGAAATATAAAAT 164958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::::|||
|65019 AAGAAAAAGAATTATAGTAATAAACATATATAATAATAATAATAGTAGTAATAAAGGTGTCC 165078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ATAGAAAAAAAAAAGTACAACAA 165174
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Ab xef="GI:2350451"
Ab xref="GI:2350451"
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Aranslation="MSTCNNIVDLVRNKKELLIGEKKWRKKSCNIDRNTIDNENNKLL
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KSABNILLKKNEYIRXLKTKLINGKALNKKALQNINNINDNIDNIDNITNISCYNLVNKODEKK
FSKHLNSSSSSSSISSYSSLSNPSDDSCPSNKQNQNNFFSNIKCNNSYFTGNAQTKNK
                                                                                     AspTyrProLysLysValAspGlyLeuThrAspGluGluAspAspAspAspGlyAspGly 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyAlaAspTyr---GluAspTyrThrAspMetLeu-------AsnLysLeu 159
                                                                                                                                                                                                                                                                                                                  GlylleAsnTyrLeuAspGluPheAspGluPheGlnLysGluTyrGluAsnAlaLeulle 105
                                                                                                                                                                                                                                                                                                                                                                                                                      LeuAspSerIleAlaAspAspGluAspAspAspValSerTyrSerSerValAspAspVal 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnAsnAlaHisThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGlu 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ProAlaProLeuHisHis 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 ArgArgArgMetHisSerArgHisArgHisLeuLeuValArgLysAlaArgSerGluAsp 269
                                                                                                                                                                                                                                                                HisLeuAspLysGluLeuLysSerLeuLysArgValValAspAsnLeuGlnGlnArgLeu 85
                                                                                                                                                                                                                                                                                164722 TCAATATTATAATGTCTAAAGAAAATATGAACAAATTAAATATGCAACCAAAA---AAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrAspSerAlaSerAlaSerAsnAspAspAsnValPheAspAspPheThrSerTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnAlaHisLysLysLysGlnGluArg-----
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164959 CATATGTCATCTAATTATGGATAAAAATATAAATCATCATGAGAATATGATAATG
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                                                                                                                                                  313050
86
80
127
120
22
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Mismatches:
Indels:
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Matches:
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40.19%
20.82%
7.77%
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Best Local Similarity:
Query Match:
DB:
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-----TCTATGAATAATAAGATTAGTAATTCAATATTGAGTAATATGAAT 165453
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T->C change at nucleotide 31605, resulting in a E->G change in
YDR470C as 113, as communicated by Hartmut Wohlrab and published in
Belenkiy, R., et al. Submitted, 2000. New Sequences and Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (27-APR-2000) Department of Genetics, Stanford University School of Medicine, Saccharomyces Genome Database, Stanford, CA
                                                                                                                                                                                                                                                                                                                                                                                                                    LeuTyrTyr------ValTyrAlaGlnIleCygTyrAgnAsnSerHis 336
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(Dases 1 to 6909)
Dietrich,F.S., Mulligan,J., Allen,E., Araujo,R., Aviles,E.,
Berno,A., Carpenter,J., Chen,B., Cherry,J.M., Chung,E., Duncan,M.,
Hunicke-Smith,S., Hyman,R., Komp,C., Lashkari,D., Lew,H., Lin,D.,
Roberts,D., Nakahara,K., Namath,A., Oefner,P., Oh,C., Petel,R.X.,
Roberts,D., Schramm,S., Schroeder,M., Shogren,T., Shroff,N.,
Winant,A., Yelbon,M., Botstein,D. and Davis,R.W.

The sequence of Saccharomyces cerevisiae chromosome IV right
270 SerArgProAlaAlaHiBPheHiBLeuSerSerArgArgArgHiBGInGlySerMetGly 289
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se Genome Database, Stanford, CA 94305-5120,
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-----AATAATGATAGGAATAACAATTCAGTGTATGATTAT
                                                                                                                                                                                                                                                                                                                         ValProThrAsnMetProHisLysValHisThrCysHisThrSerGlyLeuIle---His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeuGlnCysLeuAsnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGluArgAsnGluArgIleHisLeu---LysAspIleHisAsnAspArgAsnAlaVal
                                                                 165175 AATTTA------TTTCATATAAGTAAAGAAAATAATAAT------
                                                                                                                                      TyrHisGlyAspMetTyrIleGlyAsnAspAsnGluArgAsnSer------
                                                                                                                                                                                                                                                                             -----TyrGlnGlyHisPheGlnThrArgAspGlyValLeuThrValThrAsnThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (02-MUG-1995) Saccharomyces Genome Database,
University School of Medicine, Stanford, CA 94305, USA
Ju (bases 1 to 69009)
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Submitted (12-JUN-1997)
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Residues, Lack of Direct Relation between Consensus Residues and Transmembrane Helices, Expression Patterns of the Transport Protein Genes, and Protein-Protein Interactions with Other Proteins.
                                                                                                                  Direct Submission
Submitted (20-DEC-2002) Department of Genetics, Stanford University
School of Medicine, Saccharomyces Genome Database, Stanford, CA
                                                                                                                                                                                                                                                                                                         Direct Submission.

Direct Submission.

Submitted (14-OCT-2003) Department of Genetics, Stanford University School of Medicine, Saccharomyces Genome Database, Stanford, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neighboring Sequence:
The 5' end of this sequence contains a 1000 bp overlap with GenBank Accession Number 133007.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="YDR457W; Hect-domain-containing nprotein, required for G2/M transition; similar to Rsp5p, ORF YER125w, from SwissProt Accession Number P39940, contains motifs typical of protein kinases; CAI: 0.16"
                                                                                                                                                                                            94305-5120, USA
Delection of 16 nt (GATCCTCTTGATTTT) between 1437732 - 1437747
Sequence update by submitter
(bases 1 to 69009)
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence update by submitter
On Oct 14, 2003 this sequence version replaced gi:27316972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stanford DNA Sequence & Technology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         URL: http://genome-www.stanford.edu/e-mail: yeast-curator@genome.stanford.edu
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mol_type="genomic DNA"
ferrain="S2886; AB972"
db xref="taxon:4932"
chromosome="IV"
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mol_type="genomic DNA"
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mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        855 California Avenue
Palo Alto, CA 94304, USA
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/evidence=not_experimental
/product="Tomlp"
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/db_xref="G1:927738"
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/db_xref="taxon:4932"
/clone="cosmid 9787"
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db_xref="taxon:4932"
                                                                       5 (bases 1 to 69009)
Sethuraman, A. and Dolinski, K.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="cosmid 9410"
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                                                                                           AUTHORS
                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
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MILDLOKSDSLEKTOSRNVPYSYFKOLLSMIKNI TYSTUDIATARIANI TYSTUDIA KI SLEEQVIEDVAANYLDTGDDLPADDS GLESPEQWEKYKKLIGEDKS I YPOP MOAQYYKGCSSKELDELPFNOGLPSNI TGLESPEQWEKYKKLIGEDKS I YPOP MOAQYYKGCSSKELDELPFNOGLPSNI FTVLPPYPYPYLNA PAKTLLOLIFTKYDEP TEVFAGRILDS ILLEPLDDPATLSSLIHLFGIFTNDRY YQRASHLMQRFIEYLEKSI LPDILIRVSDS SNYSTILLAKSELPHLEELSKDVLLRYPDLSMAKYPRIPEDPMKQK INFLESS FLLLTRRFFTARNIDALIRAEINSFTARPLGGGDDAYWELTTILEEKAH VWRSPSQFIDVLCFTARFHEPDDGALVDYSIKRFLGEKDKNTQASSTEKSDIYERT GIMHLLLSQUAASEKNYYAERPREPDROGALVDYSIKRFLGEKDKNTQASSTEKSDIYERT SSYNQCKFEFLTFSRNYYAERPREPTTARFLORD SNYSCHUSEL MILALSCYLIGFLATVQDDRYTKTDVKLADDPHNNFIRKPATELSIL AKAFSDÖSGENIDLENI I IETKLNA AFVNIT FSPPQVSSKLFELDPYAFNSLTDLIS LESTKI PKELRTDALFTLECI SLKHWCSDI IRNLGGNI SHGILFQILRYI AKTLREA TDEI DEESTNUR FFYLI SULADVKPLHESLFAAGLI PTLLEI 1VSI RNCFRKTLASATH LLETFI DNSETTTRET ENDGFTMLI TSVANEI DFTLAHPETWQPPKYSVYYSI SFRE LAXIRSLKLVLKLISTDSGDRIRNLI DSPILVSLKKI LENKLVFGLTLITYTLDVVQ YIDLTTLSCKRIMQIYSYPDKRGFSLIKNLKLLFQKCALEBMYIRQHMEDSVITTETMP
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AGSGSR RSHHILHESPUNGSREPDEPVLOGI ILKSTVSRWKDI FODRY PROJECTOVI V
IPTVINRLYKVSLALQKDLENKREQEKLKNKNLLFNEAKVESHNSDA I SVEQDDI QE
SNVTHDDHEPVYVTI QGSEVDI GGTD I DDE FWALL FNDI KADVFAQHYRERRARARLN
SDHVHSRE ED BOFLEAL I PEDI LREGILLDT FARBENGRI GGSADVI RADDDVSRNDE
EVENGLIDHGANSNDRINAND PEKKKPAR I Y FAPL I DRAGI ASLAKSVF I SKPY I ORBEITY
ELFYRLCSSKQNRNDLMNTFLFILSEGI I DQHSLEKVYNI I SSRAMGHAKTTTVRQLP FGMSLGNGSFSQVPQHLEARDFLAIIFMENPPYEYFTSVAISNVTEVLQYLDEKYEDY AFMDVMKVLNDQLENLNDFLNSPNDRSFFLERDGENSVRSCHSKLCRLAAILNIVTNV SDCTPLTVANQTIEILQSLIDADSRLKYFLIAEHDNLIVNKANNKSRKEALPDKKLRW PLWHLFSLLDRKLITDESVLMDLLTRILQVCTKTLAVLSTSSNGKENLSKKFHLPSFD EDDLMKILSIIMLDSCTTRVFQQTLNIIYNLSKLQGCMSIFTKHLVSLAISIMSKLKS ALDGLSREVGTITTGMEINSELLOKFTLESSDOAKLLKILTTVDFLYTHRKEEBRNV KDLGGLYDRONGGPWASLSECLSOFEKSOAINTSATTLLETLETSTRENVCRRSDIS.SON KDTGALLDPSKTRYENLFFFTDAHKKLLNOMIRSNPKLMSGPFALLVKNPK VLDFDNKRYFENAKLKSDNOERPKLPITVRREVFLDSSKALFPKTNDEIKNSKKLEIT /timelation="MDHRNILDPKTLKVSQLRRVLVENDVAFPANARKPVLVKLFEEKV RQRQSPBASAKWFYSIQKVVKSGARVADRKKTLKSKKLESSSSSEKTVKDENVETNK RKREQISTDNEAKWOJCERESPRKKKKRSSKANKPPESPPQSKSDGKATSADLTSEL BTVEELHKKDSSDDKPRVKELPKPELPNLKVSNEFLAQLNKELASAATENYDHSIKST FKGESGVDAGGVTREWYQVLSRQMFNPDYALFLPVPSDKTTFHPNRTSGINPEHLSFF KFIGMIIGKAIRDQCFLDCHFSREVYKNILGRPVSLKDMESLDPDYYKSLVWILENDI IDIIETTSVETDDYGEHKVINLIEGGKDIIVTEANKODYVKKVVEYKLOTSVKEOMD NFLVGFYALISKOLITIFDEQELELLISGLPDIDVDDWKNNTTYVNYTATCKEVSFW RAVRSFDAEERAKLLQFVTGTSKVPLNGFKELSGVNGVCKFSIHRDFGSSERLPSSHT RHRNHHRSINRTHFHSAMSAPSLSLLNRGRRNQSNLINPLGPTGLEQVENDISDQVTV /note="similar to Saccharomyces cerevisiae hypothetical protein on chromosome XIII from GenBank Accession Number 849745, CDS number 5; CAI: 0.13" CFNQLNLPPYESYETLRGSLLLAINEGHEGFGLA" /evidence=not_experimental product="Ydr458cp" protein_id="AAB64934.1" db_xref="G1:927762" complement (10786. .12777) complement (10786. .12777) gene="YDR458C" /gene="YDR458C" codon start=1

gene

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CGEGRALFESGETTTLYTGIIPPRYKTGAKDERSKEKENDELWKYNSYLKKKNAQHE
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ETNGKREKSKSNNTYYTYRSTSKKWYTLQCHLEGDIOIVITKYGGSLFITLSDIPNIKG
ONNLMAQTKETINKEQSENIELYLEANDKKNKGEEPFLTTVQLRATLLSDIPNIKG
COMPLAGOTKETINKEQSENIELYLLEBNGEIMTCWEWKE"
/gene="YDR459C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6161 GATGAAGTTGAAGACGAGGTTGACGAGTCTGATAAGGAAGAGACTCCCGGATATGTTCAAA 6220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACTCAGCGCTG------------GGAATGTATGAGGACGTAGAA 6259
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DLSSIRIETEEPVGPSTGAETRNESEVMENINLEVQPEVKEAKEELTKISETFDNQDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6437 AGTACAGCGGACGGCACGGATGTGGACTATGAGGTTGATGATGCAGATGGACTAATTATC 6496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6674 GATTGGGACTCCGGGTTATCCAGCCTATCTATTTCTGATGAAGATAGTGAAAGTAGCGAA 6733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---AsnTyrLeuAspGluPheAspGluPheGlnLysGlu-------TyrGlu 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluAspAspAsp-----124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaHisThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluThrAsp 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerAlaSerSerAlaSerAsnAspAspAsnValPheAspAspApPhe-----ThrSer 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrAsnAlaHisLysLysLysGlnGluArgLysSerArgSerIleAlaAspValArgAsn 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValAlalleLeuAlaLeuThrIleTrpGlnThrThrArgValSerHisLeuAspLysGlu 70
                                                                                                                                                                                                                                        /gene="YDR459C"
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protein from PIR Accession Number S51289; CAI: 0.12"
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5617 GACGAGCTAAGT---TCTGGATATGATGTTGATTTAAGCGATTATGACGTAGATGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGACGACGATGACGACACCATCATTAGAGACGATGATGCTATGGCATTTGTTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6380 GCAGATGATGCTCGTTCAGATTCGGAAGAA---AATGAATTATCTTCTGAAATGCAATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuLysSerLeuLysArgValValAspAsnLeuGlnGlnArgLeuGlyIle-----
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Matches:
Conservative:
Mismatches:
Indels:
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1013 CAAAGCAACCTAATAAATTCCACTAGGGCCTACAGGTTGGAACAAGTGGAGAACGATATT 7072
                                                                                                                                                   ------GGTGAGAGTGAAGAGAT 6838
                                                                                                                                                                                                                                                                            6893 Trettragaetreargaegaaarecercaragaaacearearegecercaareaaregraee 6952
                                                                                                                                                                                                                                                LeuTyrTyrValTyrAlaGlnIleCysTyrAsnAsnSerHisAspGlnAsnGlyPheIle 342
                                                                                                                                                                                                                                                                                                            343 ValPheGlnGly-----AspThrProPheLeuGlnCysLeuAsnThrValProThrAsn 360
                                                          264 LysAlaArg---SerGluAspSerArgProAlaAlaHisPheHisLeuSerSerArgArg 282
                                                                                                                      ArgHisGlnGlySerMetGlyTyrHisGlyAspMetTyrIleGlyAsnAspAsnGluArg 302
244 ProAlaProLeuHisHisArgArgArgMetHisSerArgHisArgHisLeuLeuValArg 263
                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ArgAsnGluArgIleHisLeu 384
                                                                                                                                                                                                      AsnSerTyrGlnGlyHisPheGlnThrArgAspGlyValLeuThrValThrAsnThrGly
                                                                                                                                                                                                                                                                                                                                                                          361 MetProHisLysValHisThrCysHisThrSerGlyLeuIleHisLeuGlu-----
                                                                                       6794 GGCGTGGAGCTAACTGACGACTCGCAA-
                                                                                                                                                       TCGGAAGTT 7141
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Run on:

Scoring table:

Minimum DB Maximum DB M

Searched:

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Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; x-linked anhidrotic (hypohidrotic) ectodermal dysplasia; x-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorder; sparse hair; sweat gland aberration; endocoxic shock; inflammation; haemorrhagic necrosis of tumour; cytotoxicity; TNFv2; obesity-linked insulin resistance; gene; ds.
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Ablo6443

Ablo6443

Acd07906

Acd07906

Acd07895

Acc57577

Acc57577

Adc5223

Abl2773

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634. .1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= d
/note= "Specifically claimed in claim 22"
634. .789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding tumour necrosis factor variant 2 (TNFv2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                 ABK43159
ADC46185
ABL21925
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF82901
ABA93487
AAA70206
AAV73805
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ABL03529
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790. .1860
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misc_difference
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-Q=Cgn2_1/USFTO spool_p/USF0913339/runat_13092004_102752_21656/app_query.fasta_1.583
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-DODEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODEL=LOCAL_-OUTFWIT=PLO -NORMEREX -HEAPSIZE=500 -MININSW=0 -MAXLENS=2000000000
-USRR=US09813329_@CGN_1 1 885_@runat_1309204_102752_21656 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Abk11678 DNA encod
Abl21473 Drosophil
Abs2433 Drosophil
Abs2433 Mouse CDN
Abl15995 Drosophil
Abd76511 C. albica
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2740.557 Million cell updates/sec
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                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                                                                                  - nucleic search, using frame_plus_p2n model
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(TNF) The polypeptide and polynucleotide are useful in controlling

agriculturally important peets, particularly by modifying the growth,

feeding and/or reproduction of crop-damaging insects or insects of farm

animals. The polypeptide and polynucleotide are useful for modulating

cepithehial morphogenesis, cell-matrix adhesion in files and mammals. Thus

the polypeptide and polynucleotide may be useful for recating,

ameliorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal

cysplasia and X-linked anhidrotic (hypohidrotic) ectodermal

ike disorders, e.g. sparse hair, abnormal or missing teeth or sweat

gland aberrations in animals (e.g. insects and potentially humans),

endocoxic shock, inflammation, haemorrhagic necrosis of tumours,

cytotoxicity and obesity-linked insulin resistance, all of which involve

TNF molecules. This sequence encodes the drosophila melanogaster tumour

recosis factor variant 2 (TNFv2) protein, described in the invention
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                                                                                                                                                                                                                                             New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm animals.
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                                                                                                                                                                                             Bowen
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Matches:
Conservative:
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 /label= mature_TNFv1
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RAMANATHAN C
                                                                                                                                                                                        PM, Chen J,
                                                                                                            CARROLL P M.
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Best Local Similarity:
Query Match:
DB:
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XIAO H.
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                     US2002012968-A1
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(XIAO/)
(GUAN/)
(BOWE/)
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                                 CTCCAGCAGCGTTTGGGCATAACTATCTGGACGAGTTCGACGAGTTCCAAAAGGAGTAC
                                                                            GluAsnAlaLeuIleAspTyrProLysLysValAspGlyLeuThrAspGluGluAspAsp
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                                                           Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; epithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; sparse hair; sweat gland abbrration; endotoxic shock; inflammation; haemorrhagic necrosis of tumour; cytotoxicity; TNFv1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Drosophila tumor necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm animals.
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                                                                                                                                                                                                                                                                                      claim 18"
                                                                                                                                                                                                                                                factor variant
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                                     tumour necrosis factor variant 1 (TNFv1)
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1. 1218
/*tag= d
/note= "Specifically claimed in cl
| 1. 156
| tag= a
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                                                                                                                                         obesity-linked insulin resistance; gene; ds
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/label= mature_TNFv1
                                                                                                                                                                                          Location/Qualifiers
1. .1221
/*tag= b
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            (first entry)
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RAMANATHAN C
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GUAN B.
                                     encoding
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            05-JUN-2002
                                                                                                                                                                                                                                                                                                sig_peptide
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Sequence 1221 BP; 349 A; 323 C; 312 G; 237 T; 0 U; 0 Other

factor variant 1 (TNFv1) protein, described in the invention

necrosis

The invention describes an isolated tumour necrosis factor polypeptide (TNF). The polypeptide and polynuclectide are useful in controlling agriculturally important peets, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polynucleotide are useful for modulating the polypeptide and polynucleotide are useful for modulating the polypeptide and polynucleotide may be useful for treating, ameliorating or preventing X-linked anhidrotic (hypohidrotic) ectodermal cysplasia and X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorders, e.g. sparse hair, abnormal or missing teeth or sweat gland aberrations in animals (e.g. insects and potentially humans), condotoxic shock, inflammation, haemorrhagic necrosis of tumours, cycotoxicity and obesity-linked insulin resistance, all of which involve TNF molecules. This sequence encodes the drosophila melanogaster tumour

Claim 2; Fig 2A-B; 119pp; English.

us-09-813-329-6.rng

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       Tumour necrosis factor; TNF; pesticide; crop-damaging insect; farm animal insect; pelithelial morphogenesis; cell-matrix adhesion; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia; X-linked anhidrotic (hypohidrotic) ectodermal dysplasia. sparse hair; sweat gland aberration; endotoxic shock; inflammation; haemorrhagic necrosis of tumour; cytotoxicity; obck; inflammation; obesity-linked insulin resistance; gene; ds.
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product= "TNF"
note= "Tumour necrosis factor"
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The invention describes an isolated tumour necrosis factor polypeptide (TNF). The polypeptide and polymucleotide are useful in controlling agriculturally important peets, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polymucleotide are useful for modulating ceptchelial morphogenesis, cell-matrix adhesion in files and mammals. Thus the polypeptide and polymucleotide may be useful for treating the polypeptide and polymucleotide may be useful for treating cetodermal and x-linked anhidrotic (hypohidrotic) ectodermal dysplasial and X-linked anhidrotic (hypohidrotic) ectodermal dysplasial its disorders, e.g. sparse hair, abnormal or missing teeth or sweat gland aberrations in animals (e.g. insects and potentially humans), endocavic shock, inflammation, haemorrhagic necrosis of tumours, cytotoxicity and obseity-linked insulin resistance, all of which involve TNF molecules. This sequence encodes the drosophila melanogaster tumour necrosis factor (TNF) protein, described in the invention
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                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB273737-ABB22072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                 detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
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                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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Sequence 3324 BP; 918 A; 715 C; 681 G; 1010 T; 0 U; 0 Other;

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CAGGCAACCTAATGAAGTCACTTCTTGAATTTCTCA-GGCTACCATGGAGATATGTACAT 1344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          increasing the secretory properties of a cell, or for treating leases or conditions associated with a loss of function, e.g. diabetes
                     GACGGTGACCAATACAGGCCTATATACGTATACGCCCAGATATGCTACAACAACAACTGCA
                                                                                                                             rValproThrAsnMetProHisLysValHisThrCysHisThrSerGlyLeulleHisLe
                                                                                                                                                                                                                           GGAACGAAACGAGAGGATCCATCTGAAGGACATTCACAACGATCGCAATGCAGTTCTGCG
                                                                    uThrValThrAsnThrGlyLeuTyrTyrValTyrAlaGlnIleCysTyrAsnAsnSerHi
                                                                                                                 sAspGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeuGlnCysLeuAsnTh
                                                                                                                                                                              GGTGCCCACCAACATGCCACATAAGGTGCACACTGCCACACGAGTGGTCGTGATCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                Mouse; ss; gene, Zis-SR; neuroendocrine phenotype; diabetes; Parkinson's disease; Alzheimer's disease; neurodegenerative disease; zinc finger splicing with extended Ser-Arg domain; secretory pathway; zinc finger protein.
                                                                                                                                                                                                                                                                                1043 GGAGGGAAACAACCGAAGCTACTTTGGCATCTTCAAGGTG 1004
                                                                                                                                                                                                                                                          GGluGlyAsnAsnArgSerTyrPheGlyIlePheLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    Mouse cDNA encoding Zis-SR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Zis-SR"
                                                                                                                                                                                                                                                                                                                              ABSS4139 standard; cDNA; 2616 BP
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secretion defective cell involved in the formation of secretory granules in the Zalated polypeptide involved in the formation of secretory granules in the Zalated polypeptide involved in the formation of secretion of a cell using the mucheic acid sequence spanning amino acids 243-310 of the Zie-SR protein, restoring the neuroendocrine differentiation of a cell using the nucleic acid molecule or polypeptide cited above, identifying a gene and/or protein involved in inducing regulated cell incomprising a comparison at the molecular level of a secretion-defective cell ince under conditions that restore differentiation of the secretion-defective cell ince in the absence of the conditions cited. Also included are modulating the secretory properties of a cell comprising modulating the activity and/or level of Zie-SR and an assay to comprising modulating the activity of Zia-SR, its part or derivative in a balological activity of Zia-SR, its part or derivative in assessment of a biological activity of Zia-SR, its part or derivative in selected when the biological activity of Zia-SR, its part or derivative in measurably different in the presence of the candidate compound as compared in its absence. The nucleic acid molecules or compound as compared in its absence. The nucleic acid molecules or properties of a call, for restoring or increasing the secretory properties are useful for restoring or increasing the secretory properties of function, e.g. diabetes, neurodegenerative diseases and for long term therapies to treat diseases or conditions associated with a closs of function, e.g. diabetes, neurodegenerative diseases and as a call, for requiating diseases or conditions associated with a closs of function, e.g. diabetes or secretory pathways in cells. The nucleic acid molecules can also be used to locate gene regions associated with genetic diseases. The present sequence encodes mouse Zis-SR (zinc finger spliting compounds).

542 G; 782 T; 0 U; 0 Other; Sequence 2616 BP; 834 A; 458 C;

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2616
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                                                                    Matches:
Conservative:
Mismatches:
Indels:
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       Length:
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442 -----LeuThrAspGluGluAspAspAspAspGlyAspGlyLeuAspSerIleAla 130 AspAspGluAspAspAspValSerTyrSerSerValAspAspValGlyAlaAspTyrGlu 150 AspGluPheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLysValAspGly 113 TGTAACATGTGTAATACTCCCAAAGTATGCTAAATTÄGAAGAAGAACAGGATATGGAGGT 334 -----GluPhe 93 443 CCTGCATCTATATAAGGAAGTTGAAGATAAAGAGTCAGAGGGAGAGAA-----:::|||||||||||:::|||| GAGGATGAGGATGAAGATCTATCTAAGTATAAGCTAGAT----------IleAsnTyrLeuAsp-----335 94 131 114

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The invention relates to an isolated nucleic acid molecule, Zis-SR, encoding a protein involved in the secretory pathway in a cell(or its homologue or variant) or nucleic acid molecules that hybridise under high

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AspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHisThrGlyThrThrProThrSer 170
                                                                                                                   -----CTTGATGCCAGCGAAGAAGAAGATAGTAACAAAAGAAAGGAAATAGGCGGAGC 628
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                                                              GlnGluLysSerSerAsnGluAlaThrSerLysGluSerProAlaProLeuHisHisArg
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                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11528 BP; 2793 A; 3119 C; 3090 G; 2526 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 42467; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-00614150.
              Drosophila, developmental
pharmaceutical, gene, ss.
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                                                                  Drosophila melanogaster
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                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY
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11528 62 36 97 67 9 Length:
Matches:
Conservative:
Mismatches:
Indels: 0.0501 145.50 37.40% 23.66% 6.73% Best Local Similarity: Query Match: Percent Similarity: Alignment Scores:

x ABL15995 (1-11528) US-09-813-329-6 (1-409)

183	4 ThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluGlyGluThrAspSerAla 183	164
1669	5	161(
163	146 GlyAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHis 163	146
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145	126 LeuAspSerIleAlaAspAspGluAspAspAspValSerTyrSerSerValAspAspVal 145	126
1573	5	1535
125	106 AspTyrProLysLysValAspGlyLeuThrAspGluGluAspAspAspAspAspGlyAspGly 125	106
1534		1505
105	86 GlyIleAsnTyrLeuAspGluPheAspGluPheGlnLysGluTyrGluAsnAlaLeuIle 105	8
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85	66 HisLeuAspLysGluLeuLysSerLeuLysArgValValAspAsnLeuGlnGlnArgLeu 85	9

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Drosophila melanogaster expressed polynucleotide SEQ ID NO 42467.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid representing a synthetic BAX-gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in certain diseases.
                                                                                                                                                                                                                                                                                                  tHisSerArgHisArgHisLeuLeuValArgLysAlaArgSerGluAspSerArgProAl
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                       SerSerAlaSerAsnAspAspAsnValPheAspAspPheThrSerTyrAsnAlaHisLys
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                                                                          LysLysGlnGluArg-----
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09-JAN-2001; 2001EP-00870003
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P-PSDB; ABG93245.
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This invention describes a novel nucleic acid representing a synthetic Bax gene. The Bax gene of the invention is useful for identifying Bax-resistant yeast or fungi, identifying to obtaining and identifying Bax-candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death. The products of the invention have cytostatic, fungicide; immunosuppressive, virucide and vasctropic activity and can be used in vaccines or for gene therapy. The invention have cytostatic, fungicide; pharmaceutical compositions, antisense molecules and antibodies are useful as medicaments or in preparing a medicament for treating, preventing and/or alleviating compositions, and antibodies are useful as medicaments or in preparing a medicament for treating, preventing and/or alleviating as cancer, or for preventing apportasis in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preparing a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunishing against yeast or funding the mammals infections. Applyons-related disease, include autoimmune disease, fundant infections.
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| CAACTACTACCAATAGCAAAGATGAGTTCCAATACTCAAGATTTAGTTTTAGCTTATATT 255
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       Claim 36; Fig 2; 344pp; English.
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AGTICCGACICAAAAICIGAIICAGACICAGACICCAGCICCAGCICTGAIICA 735

PheAspAspPheThrSerTyrAsnAlaHisLysLysLysGlnGluArgLysSerArgSer 212

ThralaGluGlyGluGlyGluThrAspSerAlaSerSerAlaSerAsnAspAspAsnVal 192

173

8 8 8 8

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973 AAGTICAAAACGAGICAGAAICAICAGCAICAICTICIACIGAITCAAITCCIGCAACI 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1033 CCAGAACCAGAATTAAAGCCAGGCCAAAGAAAACAİTİTİTCTAGAATAGATAGAAGTAAA 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAGAAAAGGCTAGTGAAAATTATTACAAGTCAGAGGTAAAGATTTCACAAAGAATAAA 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------deragrarcacr 1254
                                                        -----GluGlnAsnIleGlnGly 225
                                                                                                                                                                                                                                                                                                                    GACTCTGATTCAAGTTCTGATTCCGACTCCAGCTCCAGCTCTGATTCCGACTCCAGCTCC 795
                                                                                                                                                                                                                                                                                246 ProLeuHisHisArgArgArgMetHisSerArg-----HisArgHisLeuLeuValArg 263
                                                                                                                                                                                                                                                                                                                                                                                                    ------AspSerArgProAlaAla 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----HisPheHisLeuSerSerArgArgArg 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----HisGlnGlySerMetGlyTyrHis 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asn-----GluArgAsnSerTyrGlnGlyHisPheGlnThrArgAspGlyValLeuThr 317
                                                                                                                                                                                                   Erythropoietin; EPO; G-CSF; granulocyte colony stimulating factor; wobble; codon altered gene; shuffling; modification; vaccine; insulin; peptide hormone; growth factor; cytokine; interferon; interleukin; leukaemia inhibitory factor; oncostatin M; transcription activator; expression activator; infectious organism; ds.
                                                                                                          796 AGCTCTGATTCCGATTCAGACTCAGATTCTGATAGTGACAGTGACGACAATTCCTCAGAA
                                                                                                                                                                   226 AsnHisThrGluLeuGlnGluLysSerSerAsnGluAlaThrSerLysGluSerProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---TyrileGlyAsnAsp
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                                                                                                                                                                                                                                                                                                                                                                                                 LysAlaArgSerGlu-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::
TTAGCT---AGTGGGTCCTAT 1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValThrAsnThrGlyLeuTyr 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyAspMet-----
                                                  213 IleAlaAspValArgAsnGlu--
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99US-0117729P.
99US-0118813P.
99US-0141049P.
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comprising providing a NA sequence (NA1) which encodes a polypeptide (PI), providing a NA sequence (NA1) which encodes a polypeptide (PI), providing codon altered NA sequences, each encoding 10 or a modified form of it, and recombining the codon altered NA sequences to produce a target codon altered NA which encodes a second protein. The method of the invention can be used for recombining codon-altered libraries of mucleic acids to produce new proteins, which have improvements in a desirable characteristic. Target nucleic acids include improvements in a desirable characteristic. Target nucleic acids include insulin, peptide hormones, growth factors, cytokines, interferons, interleukins, leukaemia inhibitory factor, and oncostatin M, as well as transcription and expression activators and proteins from infectious corganisms for use as vaccines. The method can also be used to produce attenuated viruses which have reduced rates of reversion to wild type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 LeuThrAspGluGluAspAspAspAspGlyAspGlyLeuAspSerlleAlaAspAspGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 AspAspPheThrSerTyrAsnAlaHisLysLysLysGlnGluArgLysSerArgSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 AlaAspValArgAsnGluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 AspAspAspValSerTyrSerSerValAspAspValGlyAlaAspTyrGluAspTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel methods for recombining codon-altered libraries of nucleic used to produce new proteins and new vectors with reduced rates o reversion to wild type.
                                                                                                                                                                                                                                                                                                                                                                                                  sequence, which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 567 BP; 32 A; 129 C; 222 G; 184 T; 0 U; 0 Other;
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                                                                                         English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum. Also described are: (I) nucleotide sequences (II) and coloridation (I) and polyclonal antibody raised (1) and polyclonal antibody raised to infection. (I) and polyclonal antibody raised to immunogens comprising the sequences of (I), are useful for the development of vaccines against P. falciparum of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum infection, or they can be used to identify drug resistance in P. falciparum sequencing of the condum chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA7078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the
                                                                                                            Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:232
                                                                                                                                          Plasmodium falciparum, chromosome 2; human malaria parasite, vaccine, antimalarial, malaria, protozoacide, infection, insecticide, ds.
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and in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines diagnosis of P.falciparum infection.
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                  AAA70099 standard; DNA; 3579
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CARUCCI D.
GARDNER M.
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2269 AGT------TIGAAAACGAAAATTATTATCCACATAATATGACATTIGGACAA 2316
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                                                                                  GATTATGAAGAAGATACAGATGATTCAGACAAAGATGTAGAACAGAAGTAGAAGAAACA 1812
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                                                                                                                                                                                                                  ------AspAspAspAspGlyAspGlyLeuAspSerIleAlaAspAspGluAsp 134
                                                                                                                                                                                                                                                                                                   135 AspAspValSerTyrSerSerValAspAspValGlyAlaAspTyrGluAspTyrThrAsp 154
                                                                                                                                                                                                                                                                                                                                                                                        155 MetLeuAsnLygLeuAsnAsnAlaHisThrGlyThrThrProThrSerGluThrThrAla 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 GluGlyGluGlyGluThrAspSerAlaSerAlaSerAsaRerAsnAsp-----AspAsnVal 192
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                                          88 AsnTyrLeuAspGluPheAspGluPheGlnLysGluTyrGluAsnAlaLeu-----
                                                                                                                               -----IleAspTyrProLysLysValAspGlyLeuThrAspGluGlu------
                                                                                                                                                                                                                                                                                                                                             1933 AAAGACAAAGAAGATGACAAAGAAGATGACAAAGAAAAAGACAAAGAGAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 ThrArgAspGlyValLeuThrValThrAsnThrGlyLeuTyrTyrValTyrAlaGlnIle
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RESULT 11 ABL06443 C

68 AspiysGluLeuLysSerLeuLysArgValValAspAsnLeuGlnGlnArgLeuGly1le 87

Indels:

Best Local Similarity:

Query Match:

US-09-813-329-6 (1-409) x AAA70099 (1-3579)

ABL06443 standard; cDNA; 6240 BP

-- AsnValPheAspAspPhe 196

733

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208 ArgiysSerArgSerIleAlaAsp------ValArgAsnGluGlu 220
                                                                                                                                                                                                                                                                                                           -----LysGluSerProAlaProLeuHisHisArgArgArgMetHisSerArgHisArg 258
                                                                                                                                                                                                                                                                                                                                                                                    259 HisLeuLeuValArgLysAlaArgSerGluAspSerArgProAlaAlaHisPheHisLeu 278
                                                                                                                                                                                                                                                                                                                                                                                                                            854 CGGCGCAGGGTGAAACCCTTTAGTTCCGAGGACAGTGATGATGACGACGCTAGCAAACGC 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; EDA1-II; X-linked hypohidrotic ectodermal dysplasia; XLHED; DL receptor; DL gene; downless gene; ectodermal dysplasia; hair follicle growth; tooth growth; endocrine sweat gland development; mammary epithelial tissue growth; breast epithelium; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a purified hypohidrotic ectodermal dysplasias protein (I) that promotes the development of hair follicles. (I) is a promoter of hair follicle growth and tooth growth. (I) is useful for the development of hair follicles. (I) is also useful for commercial and clinical diagnostic testing for ectodermal dysplasia (ED). (I) is also useful as a stimulant for hair and tooth growth, for stimulating
                                                                                                                                                                                |||||||
| CGCAAACCACCGACTGCTGTGAGAAGTCGAAAAAAGCTCCAGCACCCCAAGAACAAGAAG
                                                                                                                                                                                                                                                           794 GCCCAAAAGCGCAAACCGGCAGCAACTACCTCTCGCAGAAACTCGCACAGCAACAGCAG
                                    GCCAGCGATGCCTCTGCCGATGAATCAAGTGATGTCTGCCAATGTGTCACCCACATCC
                                                                            --- TyrAsnAlaHisLysLysLysGlnGlu
                                                                                                               TCCAGCAGCAGCAGGAGGAAGAGGAGGACTATAGACCCAAGCGGACGCCCAAGGCG
                                                                                                                                                                                                                              GlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLysSerSerAsnGluAlaThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel purified hypohidrotic ectodermal dysplasias protein, useful for promoting the development of hair follicles and tooth growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279 SerSerArgArgHisGlnGlySerMetGlyTyr 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           914 TGCGCTACTCGTCGCAAGGGTGCTGCCGTTAGCTAC 949
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Д
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CCTAAGCCGGAGCAGAATGAGGAGGAGGACAATGAGACTGAGGTCAGCAGCAGCCA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention isusful in developmental biology and in elucidaring cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                     Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811
                                                                                                                           developmental biology; cell signalling; insecticide;
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endocrine sweat gland development in individuals from whom the normal sweating mechanism is compromised by disease or surgery, for stimulating the growth of mammary epithelial tissue, either for reconstructing or cosmetic purposes, and for promoting or maintaining differentiation of breast epithelium. (I) is also useful for functional analysis, antibody production and patient therapy. ABL51009 to ABL51122 and ABB09082 to ABB09090 represent sequences used in the exemplification of the present
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The invention relates to a method of increasing or decreasing one or more of hair follicle development, tooth development, or sweat gland development, in a tissue, involves altering ectodermal dysplasia (BDA1) isoform II [BDA1-II] activity in the tissue. The method is useful for increasing or decreasing hair follicle development, tooth development or sweat gland development, in a tissue of a patient suffering from an ectodermal disease such as X-linked hypohidrotic ectodermal dysplasia (KLHED), autosomal recessive hypohidrotic ectodermal dysplasia (ABD) or alopecia. The method is useful for decreasing hair follicle development in a subject suffering from hirsutism. The method is also useful for treathing breast cancer and ectopic teeth, burns and trauma of skin due to surgery. The present sequence represents DNA encoding human EDA1-II
Increasing or decreasing hair follicle development, tooth development, or sweat gland development, in a tissue, involves modulating ectodermal dysplasia protein isoform II activity in the tissue.
                                                                                                                 Example 1; Page 59-60; 102pp; English
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Sequence 1176 BP; 271 A; 354 C; 335 G; 216 T; 0 U; 0 Other;

מ מ	acinentes	1710 DE;	2/1 A; 354 C;	335 St. 012	U; U Other;
Alignment S Pred. No.: Score: Percent Sin Best Local Query Match DB:	nent Sco No.: It Simil Local Si Match:	tt Scores: .: Similarity: al Similarity: tch:	0.0129 138.00 22.54 6.38* 8	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1176 96 57 147 127
3-60-SD	-813-329-	-6 (1-409)	x ACD07906 (1	-1176)	
δ	35		uIlePro-LeuValLe	euGlyPhelleGlyLeu	euGlyLeuValValAlaileLe 54
ą a	108		screcchecrcrrecre	GGTTTCTTTGGCCTC	AGGGAACAGCTGCTGCTTCCTGGGTTTCTTTGGCCTCTCGCTGGCCCTCCACCTGCT 167
ò	54	uAl	aLeuThrIleTrpGlnThrThrArgValSerHisLeuAspLysGluL	rArgValSerHisLeu	euLy
qq	168		GACGTTGTGCTGCTAC		CTAGAGTTGCGCTCGGA 200
ò	74		alValAspAsnLeuGlr	GlnArgLeuGlyIle	uLysArgValValAspAsnLeuGlnGlnArgLeuGlylleAsnTyrLeuAspGluPheAs 94
ΩÞ	201		GTTGCGGCGGGAACGTGGAGCCGAGTCCCGCCTTGGC-	FILLILII FICCGCCTTGGC	237
δ	94		InLysGluTyrGluAsr	ıAlaLeuIleAspTyr	pGluPheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLysValAspGlyLe 114
q ₀	237	1			237
ò	114		uThraspGluGluAspAspAspAspGlyAspGly	glyAspgly	
Ор	238		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-GGCTCGGGCACCCCT	-GGCTCGGGCACCTCTGGCACCTAAG 272
ò	127		laAspAspGluAsp	AspAspValSerTyr	-AspGluAspAspAspValSerTyrSerSerValAspAspValGl 146
οg	273		: : CAGCCTCGACCCTGACAGCCCCATCACC	AGCCCCATCACC	308
ò	146		yAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHi	MetLeuAsnLysLeu	AsnAsnAlaHisThrGly 165
οp	310				::: AGTCACCTTGGGCA 323
ολ	166		coThrSerGluThrThr	AlaGluGlyGluGly	-ThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluThrAspSerAlaSerSe 185
Ωp	324		TAAGCAGCAGCCATTG	GAACCGGGAGAAGCC	GCCGTCACCTAAGCAGCAGTTGGAACCGGGAGAAGCCGCACTCCACTTCTGACTCCCA 383
οy	185	rAlaSerAsnAsp-	1	AspAsnValPheAsp	-AspAsnValPheAspAspPheThrSerTyrAsnAl 201
Dþ	384		: ACCAGATGGCCCTATTG	::: AATTTCTTCTTCCT	GGACGGGCACCAGATGGCCCTATTGAATTTCTTCCTTCCCTGATGAAAAGCCATACTCTGA 443
٥x	201		sLysLysLysGlnGluArg	Lys	-LysSerArgSerIleAlaAsp 215
qq	444		TAGGCGTGTTCGCCGC	 !AATAAAAGAAGCAAA	AGRAGAAAGTAGGCGGTTTCGCCGCAATAAAAGAAGCAAAAGCAATGAAGGAGCAGATGG 503
ò	216	:	gAsnGluGluGlnAsn	IleGlnGlyAsnHis	-ValArgAsnGluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLysSe 234

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971 TGGATGAGAAGCCCTTCCTGCAGTGCACACGCAGCAGCAGGACAAGACCAAC---T 1027
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.028 ACAACACTTGCTATACCGCAGGCGCGCTCCTCAAGGCCCGGCAGAAGATCGCCGTCA 1087
504 CCCAGTTAAAAACAA-GAAAAAGGGAAAGGAAGGACCTCCTGGACCCAATGGCCCTC 562
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TTCCAGGAACAACTGTTATGGGACCACCTGGTCCTCCAGGTCCTCTGGTCCTCAAGGAC 682
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                          rSerAsnGluAlaThrSerLysGluSerProAlaProLeuHisHisArgArgArgMetHi
                                                      cagaaccccaagaccrccaggaccccaggaacccccaggaarrccaggaarrccrggaa
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                                                                                     sSerArgHisArg---HisLeuLeuValArgLysAlaArgSerGluAspSer----
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                                                                                                                                                                                                                       The present invention describes a purified hypohidrotic ectodermal dysplasias protein (I) that promotes the development of hair follicles. (I) is a promoter of hair follicle growth and tooch growth. (I) is useful for the development of hair follicles (I) is also useful for commercial and clinical diagnostic testing for ectodermal dysplasia (ED). (I) is also useful as a stimulant for hair and tooth growth, for stimulating endocrine sweat gland development in individuals from whom the normal sweating mechanism is compromised by disease or surgery, for stimulating the growth of mammary epithelial tissue, either for reconstructing or cosmetic purposes, and for promoting or maintaining differentiation of breast epithelium. (I) is also useful for functional analysis, antibody production and patient therapy. ABL51009 to ABL51122 and ABB0908 to
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The invention relates to a method of increasing or decreasing one or more of hair follicle development, tooth development, or sweat gland development, in a tissue, involves altering ectodermal dysplasia (BDA1) isoform II [BDA1-II] activity in the tissue. The method is useful for increasing or decreasing hair follicle development, tooth development or sweat gland development, in a tissue of a patient suffering from an ectodermal disease such as X-linked hypohidrotic ectodermal dysplasia (KLHED), autosomal recessive hypohidrotic ectodermal dysplasia alopecia. The method is useful for decreasing hair follicle development in a subject suffering from thirtism. The method is also useful for treating breast cancer and ectopic teeth, burns and trauma of skin due to surgery. The present sequence represents CDNA encoding human EDA1-II
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146 yAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHisThrGly--
                            ----AGTCACCTTGGGCA
                                                                                 565 GCCGTCACCTAAGCAGCAGCCATTGGAACCGGGAGAAGCCGCACTCCACTCTGACTCCCA
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Sequence 14, Application US/09342681C

Patent No. 6355782

GENERAL INFORMATION:
APPLICANT: Zonana et al.
TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
FILE REFERENCE: 52978

CURRENT APPLICATION NUMBER: US/09/342,681C

CURRENT FILING DATE: 1998-06-29

PRIOR PILING DATE: 1998-07-09

PRIOR PILING DATE: 1998-12-15

NUMBER OF SEC ID NOS: 123

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 14

LENGTH: 1176
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Sequence 3, Appli
Sequence 37, Appli
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Sequence 1481, Ap
Sequence 25, Appl
Sequence 32, Appl
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US-08-971-089-3
S14034-3
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US-09-106-343A-1
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US-09-136-393A-7
US-09-136-937-7
US-09-136-937-7
US-09-136-937-7
US-09-136-938-54-829
US-09-252-991A-829
US-08-338-534-25
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US-08-38-544-21
US-08-288-442-10
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cqn2 1/087PT0 spool.p/USO813329/runat 13092004 102753 21701/app_query.fasta_1.583
-Q=/Cqn2 1/087PT0 spool.p/USO8813329/runat 13092004 102753 21701/app_query.fasta_1.583
-DB=189u6d_Patents NA -QFMT=fastap -SUFFIX=rni -MIÑMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=PED -NOME=ext -HEAPSIZE=500 -MINIEN=0 -MAXENE=200000000
-USER=USO9813329 @CGN 1 1 128 @runat 13092004 102753 21701 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NEG SCORES=0 -WAIT - 18SPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                               September 15, 2004, 06:59:38 ; Search time 103 Seconds
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11. /cgn2_6/prodate/2/ina/5A_COMB.seq:*
12. /cgn2_6/prodate/2/ina/5B_COMB.seq:*
31. /cgn2_6/prodate/2/ina/6B_COMB.seq:*
41. /cgn2_6/prodate/2/ina/6B_COMB.seq:*
42. /cgn2_6/prodate/2/ina/PCTUS_COMB.seq:*
43. /cgn2_6/prodate/2/ina/PCTUS_COMB.seq:*
44. /cgn2_6/prodate/2/ina/PCTUS_COMB.seq:*
45. /cgn2_6/prodate/2/ina/PcTUS_COMB.seq:*
65. /cgn2_6/prodate/2/ina/backfiles1.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                  - nucleic search, using frame_plus_p2n model
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US-09-342-681C-1
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US-09-298-568-1
US-09-757-669A-20
US-09-757-669A-20
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Listing first 45 summaries
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CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION UNMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
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Patent No. 6673549

Patent No. 673549

Patent Butch Application September 1

APPLICANT: Buchbinder, Jenny

TITLE OF INVENTON: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS PILE REFERENCE: PA-0041 US
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|1032 ATGATCTTTCAGGTGGAGTGCTCAATGACTGGTCTCGCATCACTATGAACCCCAAGGTGT 1091
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                                                                                                                                                                                                                                                                                        201 aHisLysLysLysGlnGluArg-------LysSerArgSerIleAlaAsp-- 215
                                                                                                                                                                                                                                                                                                                                                                                                                                    803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 yrAlaGin-----IleCysTyrAsnAsnAsnSerHisAspGlnAsnGlyPheIleValPheG 345
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    yAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHisThrGly-- 165
                                                                                          166 -ThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluThrAspSerAlaSerSe 185
                                                                                                                                                                                                                          GACGGCCCAGATGGCCCTATTGAATTTCTTCCTGATGAAAAGCCATACTCTGA 684
                                                                                                                                                                                                                                                                                                                                                                                  ----ValArgAsnGluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLysSe 234
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864 TTCCAGGAACAACTGTTATGGGACCACCTGGTCCTCCAGGTCCTCCTGGTCTCAAGGAC 923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 lyAspMetTyrIleGly-----AsnAspAsnGluArg-----AsnSerTyrGlnG 307
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                                                                                                                                                                                          rAlaSerAsnAsp------AspAsnValPheAspAspPheThrSerTyrAsnAl 201
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                                                 --AGTCACCTTGGGCA
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     US-09-813-329-6 (1-409) x US-08-728-323A-1 (1-3489)
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Patent No. 6322792
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                     -----GluAspSerArgProAlaAlaHisPheHisLeuSerSerArgArgArgHisGln 285
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APPLICANT: Chang, Yuan
APPLICANT: Bobenzky, Roy A.
APPLICANT: Bobenzky, Roy A.
APPLICANT: Bobenzky, Roy A.
APPLICANT: Bobenzky, Roy A.
APPLICANT: Busso, James J.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & Dunham LLP
                                                               251 ArgArgMetHisSerArgHisArgHisLeuLeuValArgLysAlaArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELECOMMUNIC: 212-278-0400
TELEFAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
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Conservative:
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STREET: 1185 Avenue of the Americas
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Patent No. 5948676
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STATE: New York
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MOLECULE TYPE:
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APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RIADINO VIRUS DAN TO MEDIATE EFFICIENT EPISOME PERSISTENCE
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REPERBENGE: 16412-10001R
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,422
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
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          Length:
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Patent No. 6482587
GENERAL INFORMATION:
APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or E
TITLE OF INVENTION: Methods to Inhibit or E
TITLE OF INVENTION: Mothods to Jaya
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.0
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Best Local Similarity:
Alignment Scores:
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                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                            sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                              US-09-813-329-6 (1-409) x US-09-410-399-1 (1-3489)
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                                                                                                                     0.000405
133.00
35.47%
25.21%
6.15%
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                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                          Карові'в
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LENGTH: 3489
TYPE: DNA
ORGANISM: Kap
                                                                                                        Alignment Scores:
Pred. No.:
                      ; TYPE: DNA
; ORGANISM: Kar
US-09-410-399-1
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20685 ATCCAAAGTTCACAACAGCAGCAGAGCCACAAACAGGAGCCACAGAGCAGGAGCCA 20626
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                                                                                                                                                                           rArgHisArgHisLeuLeuValArgLysAlaArgSerGluAspSerArgProAlaAlaHi 275
            ---GluLeuGlnGlu-LysSer---SerAsnGluAlaTh 239
                                                                                              ------HisArgArgMetHisSe
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                                                                                                                                                                                                                                                         275 BPheHisLeuSerSerArgArgArgHisGlnGlySerMetGlyTyrHisGlyAspMetTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chang, Yuan
APPLICANT: Chang, Yuan
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidare S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  20448 CAGGAGCCACAGAGCAGCACACAGCAGCAGCACC 20409
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669A
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                          239 rSerLysGluSerProAlaProLeuHis--
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                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-757-669A-20/c
; Sequence 20, Application US/08757669A
Patent No. 6183751
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENY INFORMATION:
MAHLE, JOHN P.
REGISTRATION NUMBER: 28,678
REFREENCE/POCKET NUMBER: 4518
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
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nucleic acid
EDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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: U.S.A.
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Best Local Similarity:
Query Match:
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STREET: 118
CITY: New Y
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Pred. No.:
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      POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
                                                                                                                      CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
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Matches:
Conservative:
Mismatches:
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                                                                                     ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 5234
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 32207 base pairs
nucleic acid
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35.47%
25.21%
6.15%
TITLE OF INVENTION: POL
TITLE OF INVENTION: HER
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & D
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STRANDEDNESS:
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Patent No. 569866
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stage, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20448 CAGGAGCCACAGCAGCAGCACACAGCAGCAGCACCAC 20409
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                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                               Alignment Scores:
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                                                                       GATGACGAGGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGATGACGAGGAG
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APPLICANT: Bohenzky, Roy A
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S
APPLICANT: Edelman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNEUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: 45185-G-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,371A
CURRENT FILING DATE: 1999-11-17
PRIOR PAPLICATION NUMBER: PCT/US97/13346
PRIOR FILING DATE: 1997-07-22
                                          AspGluPheAspGluPheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLys 110
                                                                                                                                  111 ValAspGlyLeuThrAspGluGluAspAspAspAspAspGlyAspGlyLeuAspSerIleAla 130
                                                                                                                                                                                                                                                                                                                    AspTyrThrAspMetLeuAsnLysLeuAsnAsnAlaHisThrGlyThrThrProThrSer 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 ArgSerIleAlaAspValArgAsnGluGluGlnGlnAsnIleGlnGlyAsnHisThr---- 228
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                                                                                                                                                                             20967 GATGACGAGGATGACGAGGATGACGAGGAGGATGACGAGGAGGATGACGAGGAG
                                                                                                                                                                                                                          AspAspGluAspAspAspValSerTyrSerSerValAspAspValGlyAlaAspTyrGlu
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US-09-813-329-6 (1-409) x US-08-757-669A-20 (1-32207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/09230371A Patent No. 6348586
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SOFTWARE: Patentin Ve
SEQ ID NO 20
LENGTH: 32207
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US-09-230-371A-20/c
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558 TCAGGCACTACTACTACACAACAGGGCTATCGTTTAAATTCAAAAAGAGGACGACGGC 1617
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     177 GluGlyGluThrAspSerAlaSerSerAlaSerAsnAspAspAsnValPheAspAspPhe 196
                                                                                                                                                         216 ValArgAsnGluGluGlnAsn-----1leGln 224
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                                                                             ThrSerTyr---AsnAlaHisLysLysLysGlnGluArgLysSerArgSerIleAlaAsp
                                                                                                                 618 ATTAGTTTTGGTAATGGTAATGAAGGCTATAACGAGGATATAGGTGAAGAAGTCTTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/08938534
Patent No. 5916752
GENERAL INFORMATION:
APPLICANT: Gottschling, Daniel E.
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Compositions and Methods
NUMBER OF SUQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,534
FILING DATE: 26-SEP-1997
CLASSIFICATION: 536
PROOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,080
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77210
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MEDIUM TYPE: Floppy
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STREET: P.O. Bo
CITY: Houston
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73
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                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILING DATE: CONCURRENTLY Herewith
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                            ARCD:155/PAR
                                                                                                                                                                                               PRIOR APPLICATION DATA

APPLICATION DATA:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
CLASSIFICATION: S14
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERNCE/DOCKET NUMBER: ARCD:155/PJ
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 AspValGlyAlaAspTyrGluAsp-----
UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4599 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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32.97%
19.89%
5.97%
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               ZIP: 77210
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
DB:
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US-08-431-080-27
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                                                                                                                                                                                                   2023 TACAATCAAGAAAACGGATATGATGAAGAAGATGACGAAGAAGATGAAATAATGTCTGAT 2082
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                                                                                                                265 AlaArgSerGluAspSerArgProAlaAlaHisPheHisLeuSerSerArgArgHis 284
                                               245 AlaProLeuHisHisArgArgArgMetHisSerArgHisArgHisLeuLeuValArgLys
 Singer, Miriam S.

TITLE OF INVENTION: Telomerase Compositions and Methods NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSER: Arnold, White & Durkee

STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 30-Jun-1999
CLLASSIPTCATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,080
ATORILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: TEXAS COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/345,294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2083 TTTGATATGCCGTTTTATGAA 2103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 27, Application US/09345294; Patent No. 6387619
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4599 base pairs
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STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                300 AsnGluArgAsn----
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.678 TTAAAAACAAAGAGAACAATGCTAATGAAGAAGATAAACTGGATTCTAAGGTGATGTTA 1737
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-813-329-6 (1-409) x US-08-938-534-27 (1-4599)
             ATONEY/AGENT INFO...

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: ARCD:155/PAR

TELECOMMUNICATION INFORMATION:
TELEFAX: (713) 789-2679

TELEFAX: 79-0924

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERICS:
LENGTH: 4599 base pairs
TYPE: nucleic acid

TYPE: nucleic acid

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspValGlyAlaAspTyrGluAsp-------
                                                                                                                                                                                                                                                                                                               Length:
Matches:
 SN 08/326,781
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32.97%
19.89%
5.97%
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                              gnment Scores:
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1678 TTAAAAACAAAGAGAACAATGCTAATGAAGAAGATAAACTGGATTCTAAGGTGATGTTA 1737
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; SEQUENCE DESCRIPTION: SEQ ID NO: 27: US-09-345-294-27
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	СD	2023 TACAATCAAGAAAACGGATATGATGAAGAAGATGAAGAAGAAGAAGAAGAAGAAG
	à	346 GlyAspThrProPheLeuGln 352
	QQ	2083 TTIGHTHIGCGTTTTATGAR 2103
	RESULT 1 US-08-95	13 56-171E-39
	; Sequer; ; Patent ; GENE	; Sequence 39, Application US/U89501/1E 2 Patent No. 6593114 ; GENERAL INFORMATION:
		APPLICANT: Charles Kunsch Gil H. Choi
	. •- •-	Patrick S. Dillon Craiq A. Rosen
		. sg.
		ONDENCE ADDRESS:
	·- ·-	ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
		CITY: Rockville STATE: Marvland
	. •. ·	COUNTY USA
		FORM:
		MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
	. •- •	OPERATING SYSTEM: MSDOS version 6.2
		APPLICATION NUMBER: US/08/956,171E FILING DATE: 20-Oct-1997
		CLASSIFICATION CORNOWINS
		PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/009,861
	. •• •	FILING DATE: January 5, 1996 APPLICATION NUMBER: 08/781 986
		FILTER DATE: January 3, 1997
		AIIOKNEI/AGENI INFORMATION: NAME: Mark J. Hyman
		REGISTRATION NUMBER: 46,789
		TELECOMMUNICATION INFORMATION:
		HONE: (240) 3 AX: (301) 309
	INFO	INFORMATION FOR SEQ ID NO: 39; SECURNCE CHARACTERISTICS:
		MINISTER 1452
		TYPE: nucleic acid STRANDEDNESS: double
	9	SEQUE
	08-80-80	00-1/1E-34
	Alignment : Pred. No.:	cores: 0.00187
	Score: Percent (128.50 Matches: 30.25% Conservative:
	Best Loca	imilarity: 18.25% Mismatches:
	Query Match: DB:	5.94% Indels: 4 Gaps:

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Sequence 15, Application US/09485077A

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Sequence 15, Application US/09485077A

Sequence 15, Application US/09485077A

Sequence 15, Application

Sequence 15, Application

Sequence 15, Application

Sequence 15, Application

TITLE OF INVENTION: Methods and Compositions for Treatment of Restenosis

FILE REFERENCE NIH-05047

CURRENT APPLICATION NUMBER: US/09/485,077A

CURRENT FILING DATE: 1998-07-08

PRIOR FILING DATE: 1998-07-08

PRIOR FILING DATE: 1997-07-08

SEQ ID NOS: 18

SOFTWARE: Patentin Version 3.0

SEQ ID NO 15.
                                                                                                                    3295 AATATGACATCAAACAATGTTGAGAACAATCAACTTATTGGTCATGCAGAAACAGAAAAT 3354
3175 CCTGBATTAAAGCCTGTACAAAGTAAGCAAGCTGTGAGTGAAAGAATGCCTGCGAGTCAA 3234
                                                               3235 GCCACACCATCATCAAGATCTGATTCACAAGAGTCAAATACAAATGCATATAAAAACAAAT 3294
                                276 PheHisLeuSerArgArgArgArgHisGlnGlySer----MetGlyTyrHisGlyAsp 293
                                                                                             294 MetTyrIleGlyAsnAspAsnGluArgAsnSerTyrGlnGlyHisPheGlnThrArgAsp 313
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                                                                                                               TCCAACGAAAGCCATGACCATGGATGGATGGATGATGAAGATGATGATGATGTGTG
                                   AspGluPheAspGluPheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLys
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                                                      GAAGAAACCAATGACTTTAAACAAGAG---
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                                        152 TyrThrAspMetLeuAsnLysLeu-----AsnAsnAlaHieThrGlyThrThrProThr 169
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523 GTAGAC---ACATATGATGGCCCAAGGTGATAGTGTGGTTTATGGACTGAGGTCAAAATCT 579
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------AATGATGAGAGCAAT-----GAGCATTCCGATGTGATAGTCAG 858
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                                                                       463 GTCACTGATTTTCCCACGGACCTGCCAGCAACCGAAGTTTTCACTCCAGTTGTCCCCACA
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Parent No. 6551990

GENERAL INFORMATION:
APPLICANT: Giachelli, Cecilia M.
APPLICANT: Steitz, Susie
TITLE OF INVENTION: Methods of Inhibiting Ectopic Calcification
FILE REFERENCE: P-UW 3244
CURRENT APPLICATION NUMBER: US/09/206,576
CURRENT FILING DATE: 1998-12-07
NUMBER OF SEQ ID NOS: 10
SOFTWARR: PatentIn Ver. 2.0
SSEQ ID NO 1
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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22.76%
5.62%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 45792, A Sequence 46034, A Sequence 447, App

Sequence 447, App Sequence 52112, A Sequence 81649, A Sequence 7734, App Sequence 14, Appli Sequence 1, Appli

6, Appli 45, Appl 24791, A 19, Appl

Sequence 14 Sequence 1, Sequence 4, Sequence 6, Sequence 6, Sequence 245 Sequence 245 Sequence 245

Sequence 19, Appl Sequence 271, App Sequence 19, Appl

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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Total number

Searched:

Minimum DB e Maximum DB e

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Segent No. US20020012968A1
Segent No. US20020012968A1
GENERAL INFORMATION:
APPLICANT: Britatol-Myers Suibb Company
TITLE OF INVENTION: Variants Thereof
TITLE OF INVENTION: Variants Thereof
TITLE OF INVENTION: Variants Thereof
TITLE NEFERENCE: D0016.np
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR APPLICATION NUMBER: 60/190,816
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Version 3.0
SEQ ID NOS: 65
SEQ ID NOS: 65
                                                                                                1 US-10-437-963-45792
3 US-10-437-963-45792
3 US-10-437-963-46034
3 US-10-437-963-81649
3 US-10-437-963-82112
3 US-10-437-963-82112
3 US-10-437-963-82114
4 US-09-729-658B-14
6 US-00-729-658B-14
7 US-10-20-062-41
8 US-10-20-062-41
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; NAME/KEY: CDS
; LOCATION: (634)..(1860)
US-09-813-329-5
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-MODEL=frame+ pin.model -DEV=xlp
-MODEL=frame+ pin.model -DEV=xlp
-Q=/Cgn2 1/USPTO spool p/US09813329/runat_13092004_102755_21784/app_query.fasta_1.583
-Q=/Cgn2 1/USPTO spool p/US09813329/runat_13092004_102755_21784/app_query.fasta_1.583
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MIRMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPRY=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXEN=200000000 -USER=US09813329 @CGN 1 1 912 @runat 13092004 102755_21784
-NCPU=5 -NORM=0 -NARN TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -XGAPDF=10 -X
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                                                                                                                                                                                                        September 15, 2004, 10:23:37; Search time 744 Seconds
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1 MTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV
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(1902 6) ptodata 2/pubpna/US07 PUBCOMB. seq:*
(1902 6) ptodata 2/pubpna/US06 PUBF PUB. seq:*
(1902 6) ptodata 2/pubpna/US06 PUBF PUB. seq:*
(1902 6) ptodata 2/pubpna/US06 PUBCOMB. seq:*
(1902 6) ptodata 2/pubpna/US07 NEW PUB. seq:*
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(1902 6) ptodata 2/pubpna/USS0 NEW PUB. seq:*
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(1902 6) ptodata 2/pubpna/USS0 NEW PUB. seq:*
   GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                                                                                                                                     nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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is derived by analysis of
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Match Length DB
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Database :

Score

Result

and is

Sequence 2682, Ap Sequence 2682, Ap Sequence 16858, A

Sequence 7653, P Sequence 95869, 6546,

Sequence Sequence 1 Sequence Sequence

Sequence 39, Appl Sequence 61685, A Sequence 6421, Ap Sequence 8857, Ap Sequence 22862, Ap Sequence 4557, Ap

Sequence 1, Appli Sequence 1, Appli Sequence 107179, Sequence 69258, A Sequence 6017, A Sequence 58, Appl

Db 1534 GAGGAAACTCTTATCAGGGACACTTTCAAAC Qy 321 ThrGlyLeuTyrTyrValTyrAlaGlnIleCy	Oy 361 MetProHisLysValHisThrCysHisThrSe	Qy 381 ArgileHisLeuLysAspileHisAsnAspAr 	Qy 401 ArgSerTyrPheGlyllePheLyeVal 409	RESULT 2 US-09-813-329-3 ; Sequence 3, Application US/09813329 ; Patent No. US20020012968A1	; GENERAL INFORMATION: ; APPLICANT: Bristol-Myers Suibb Company ; TITLE OF INVENTION: No. US20020012968Alel D: ; TITLE OF INVENTION: Variants Thereof	; FILE REFERENCE: DOO16.np ; CURRENT APPLICATION NUMBER: US/09/813,329 ; CURRENT FILING DATE: 2001-03-20 ; PRIOR APPLICATION NUMBER: 60/190,816	; PRIOR FILING DATE: 2000-03-21 ; NUMBER OF SEQ ID NOS: 65 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 3	LENGTH: 1 TYPE: DNP ORGANISM: FEATURE:	0-0		Best Local Similarity: 96.39\$ Mismatch Query Match: 96.32\$ Indels: DB: 9 Gaps:	US-09-813-329-6 (1-409) x US-09-813-329-3 (1-12 Qy 1 MetThrAlaGluThrLeuLysProPheIleThr	Db 1 ATGACTGCCGAGACCCTCAAGCGTTTATAACC Qy 21 ProAlaLysAlaThrSerThrafthrAlaGln	61	121 GTTTTGGGGTTCATCGGGTTGGGGCTGGTCGTT QY	Db 181 ACAACGCGTGTATCGCATCTGGACAAGGAGCTG Qy 81 LeuGlnGlnArgLeuGlyIleAsnTyrLeuAsp
Alignment Scores: Pred. No.: Score: Score: Best Local Similarity: DB:: US-09-813-329-6 (1-409) x US-09-813-329-5 (1-2148)	1 Methraladluthrieulysprophe: 	ThralaThralaGlnArgArgThrargGlnLeuileFroLeu		Qy 61 ThrThrargValSerHisLeuAspLysGluLeuLysSerLeuLysArgValValAspAsn 80	Qy 81 LeuGlnGlnArgLeuGlylleAsnTyrLeuAspGluPheAspGluPheGlnLysGluTyr 100 ll	Oy 101 GluasnalaLeuileAspTyrProLysLysValAspGlyLeuThrAspGluGluAspAsp 120	Qy 121 AspAspGlyAspGlyLeuAspSerIleAlaAspAspGluAspAspAspValSerTyrSer 140	Oy 141 SerValAspAspValGlyAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsn 160 	Qy 161 AsnAlaHisThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluThr 180 Db 1114 AATGCACATACCGGCACCACCACATACTGAGACCACATGTTGAGGGCGAGACG	erAsnAspAspAsnValPheAspAspPheThrSerTyrAsn 	Qy 201 AlaHisLysLysLysLysLysLysSerArgSerIleAlaAspValArgAsnGluGlu 220	Qy 221 GlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLysSerSerAsnGluAlaThrSer 240		erdludspSerArgProAlaAlaHisPheHisLeuSerSer 	QY 281 ArgargargHisGlnGlySerMetGlyTyrHisGlyaspMetTyrIleGlyasnAspAsn 300 Db 1474 AGGCGGCGTCACCAAGGAAGTATGGCCTACCATGGAGATATGTACATAGGAAATGATAAC 1533	

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Drosophila Tumor Necrosis Factor Class Molec
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CGCGCGATGGCGTCTTGACGGTGACCAAT 1593
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GAGAATGCCCTCATCGACTATCCAAAAAAGGTGGATGGCCTCACGGATGAGGAGGAGGACGAC
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                                                                    AspAspGlyAspGlyLeuAspSerIleAlaAspAspGluAspAspAspAspValSerTyrSer
                                                                                GACGATGGCGATGGTCTGGATTCCATTGCGACGACGACGACGACGACGTTAGCTATAGC
                                                                                                          ServalAspAspvalGlyAlaAspTyrGluAspTyrThrAspMetLeuAsnLysLeuAsn
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                              GluAsnAlaLeuIleAspTyrProLysLysValAspGlyLeuThrAspGluGluAspAsp
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; Sequence 1, Application US/09813329 Patent No. US20020012968A1 ; GENERAL INCRMATION: ; APPLICANT: Bristol-Myers Suibb Company

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INVENTION: No. US20020012968Alel Drosophila Tumor Necrosis Factor Class
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TITLE OF INVENTION: No. US20020012968A1el Dr
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.np
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
FRIOR FILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                    TYPE: DNA
ORGANISM: Drosophila melanogastor
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96.82%
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US-09-813-329-1
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Best Local Similarity:
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Sequence 46034, Application US/10424599
Sequence 46034, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
BAPLICANT: La Rosa Thomas J
APPLICANT: Each Vihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53-23)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 46034
LENGTH: 1269
TYPE: DNA
                                                                                          1411 CTCACCTACTTCGAGTACCGCCGCGTCAAGAGA---GAGAAGCTCCGCAAGAGCATGAAG 1355
                                                                                                                                                        1102 CGTAGCAGCAAGCGTAGCCGCCACCACCATTCATCATCATACAGAGGTGAC 1043
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; Publication No. US20040123343A1
; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yongwei
    APPLICANT: Cao, Yongwei
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Buckharov, Andrey A.
    APPLICANT: Li, Phng
    APPLICANT: Li, Phng
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    FILE REPERENCE: 38-21(5321)B
    CURRENT APPLICATION NUMBER: US/10/437,963
    CURRENT FILING DATE: 2003-05-14
    NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                 1612 GCAGGCCTATATTACGTATATGCGCCTACAACTTCGCACCACCACGAACGGA 1671
                                                                                          AAAGAGAGCCTGCAGCACTTCACCTCCGTCGCAGAATGCATTCCCGCCATCGCCACCTC 1431
                                                                                                                                                             GTAGTCCGCAAAAGCCAGATCCGAGGACTCGAGGCCAGCAGCCCATTTCCACTTGAGCAGC 1491
                                                                                                                                                                                                                         ArgArgArgHisGlnGlySerMetGlyTyrHisGlyAspMetTyrIleGlyAsnAspAsn 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1732 ATGCCACATAAGGTGCACACCTGCCACACGGTGGTCTGATCCACCTGGAACGAAACGAG 1791
                                                        LysGluSerProAlaProLeuHisHisArgArgArgMetHisSerArgHisArgHisLeu 260
                                                                                                                                                                                                                                                                                                                                                ThrGlyLeuTyrTyrValTyrAlaGlnIleCysTyrAsnAsnAsnSerHisAspGlnAsnGly 340
CAGAATATTCAAGGAAATCACACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAGCTTCC
                                                                                                                             LeuValArgLysAlaArgSerGluAspSerArgProAlaAlaHisPheHisLeuSerSer
                                                                                                                                                                                                                                                                        GluArgAsnSerTyrGlnGlyHisPheGlnThrArgAspGlyValLeuThrValThrAsn
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Gaps:
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US-10-437-963-45792
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6.73$
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ORGANISM: Oryza sativa
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Best Local Similarity:
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CTCCGTTTGTTTGCGGAACAACGAGTTTCGAAATCCCGTGGAGAACGTAACATTCTTTGG 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 ThrGlyThrThrProThrSerGluThrThrAlaGluGlyGluGlyGluThrAspSerAla 183
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                                                                                                                                                                                                                                                                                    ------LeuValLeuGlyPheIleGlyLeuGlyLeuValValAlaIleLeuAla
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Matches:
Conservative:
Mismatches:
Indels:
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           ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_14156C.1
US-10-424-599-46034
                                                                                 143.00
35.69%
22.15%
6.61%
                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
ORGANISM: Glycine
                                                           Alignment Scores:
Pred. No.:
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Sequence 47, Application US/10451467A

| Sequence 47, Application US/10451467A
| Publication No. US20040161840A1
| GENERAL INFORMATION:
| APPLICANT: CONTRERS, ROLAND HENRI
| APPLICANT: EBERHARDY, INES
| APPLICANT: REBERHARDY, INES
| APPLICANT: RESERVANS, RIERA JOSEPHINA
| TITLE OF INVENTION: YEAST AND FUNG!
| TITLE OF INVENTION: YEAST AND FUNG!
| FILE REFERENCE: JAB-1667
| CURRENT APPLICATION NUMBER: EP 00870318.3
| PRIOR FILING DATE: 2000-12-22
| PRIOR FILING DATE: 2001-01-04
| PRIOR PLICATION NUMBER: EP 01870002.1
| PRIOR PRILICATION NUMBER: EP 01870003.9
| NUMBER OF SEQ ID NOS: 732
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 447
| TUBENTH: LEB FERENCE: LEB OF SEQ ID NOS: 732
| SEQ ID NO 447
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                                                                          256 AATGATTATGTTTCCAGAAATGAAGAATTGTCAAAGTTGAAGAGGCATTATCGAAATTC 315
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326 GGCGAGGAGGAGGAAGAAGATGTCGATGATGATGGTGAGAAGTCTGAGGCTCCACCA 885
                                               280 rargargarghisginglySerMetGlyTyrHisGlyAspMetTyrIleGlyAsnAspAs 300
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Should R
APPLICANT: About Vibra
APPLICANT: About Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 1057
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                                                                                                                                                                                                                                                                                                                                                           135 AspAspValSerTyrSerSerValAspAspValGly---AlaAspTyrGluAspTyrThr 153
                                                                                                                                                                                                                                                                                                                                                                                                                                          174 AlaGluGlyGluGlyGluThrAspSerAlaSerSerAlaSerAsnAspAspAsnValPhe 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 AspAspPheThrSerTyrAsnAlaHisLysLysLysGlnGluArgLysSerArgSerIle 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 AlaAspValArgAsnGluGluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLys 233
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ORGANISM: Glycine max
FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_44746C.1
US-10-424-599-81649
                ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_5443C.1
US-10-437-963-52112
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Publication No. US20040031072A1
GENERAL INFORMATION:
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    ORGANISM: Oryza sativa
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|1153 GGAGAAAAGGCTAGTGAAAATTATTACAAGTCAGAGGTAAAGATTTCACAAAGAATAAA 1212
                                                                                                        ThralaGluGlyGluGlyGluThrAspSerAlaSerSerAlaSerAsnAspAspAsnVal 192
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                                             AspMetLeuAsn---LysLeuAsnAsnAlaHisThrGlyThrThrProThrSerGluThr 172
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                                                                                                                                                                                                                                                                                                                LysAlaArgSerGlu------AspSerArgProAlaAla 274
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Publication No. US20040123343A1
GENERAL INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Roy Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Publication No. US20040034888A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Schou, Yihua
APPLICANT: Schou, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Row Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313)B
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                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-425-114-7734
Alignment Scores:
Pred. No.:
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Matches:
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                                                                                                                                                     ; OTHER INFORMATION: Clone ID: 700727423_FLI
US-10-425-114-7734
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
LENGTH: 966
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Best Local Similarity:
Query Match:
DB:
                                                                                                       TYPE: DNA ORGANISM: Glycine
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Pred. No.:
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sequence 1, Application US/09729658B
sequence 1, Application US/09729658B
publication No. US20030023991A1
GENERAL INFORMATION:
APPLICANT: Zonana et al.
TILLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
FILE REFERENCE: 55924 Hypohydrotic ectodermal dysplasia genes and proteins
FILE REFERENCE: 55924 Hypohydrotic ectodermal dysplasia genes and proteins
CURRENT APPLICATION NUMBER: US/09/729, 658B
CURRENT FILING DATE: 1999-06-29
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/112,366
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
TYPE: DNA
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444 AGAAGAAGTGGGGTGTTCGCCGCAATAAAAGAAGCAAAGCAATGAAGGAGCAGATGG 503
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----LysSerArgSerIleAlaAsp--
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i Sequence 14, Application US/09729658B

i Sequence 14, Application US/09729658B

i Publication No. USZ0030023991A1

i Publication No. USZ0030023991A1

i PRICANT: Zonana et al.

i TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins

i TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins

i FILE REPERENCE: 55924

i CURRENT APPLICATION NUMBER: US/09/729,658B

i CURRENT FILING DATE: 1099-06-29

i PRIOR FILING DATE: 1999-06-29

i PRIOR FILING DATE: 1998-07-09

i PRIOR FILING DATE: 1998-07-09

i PRIOR FILING DATE: 1998-12-15

i SOFTWARE: PatentIn Ver. 2.1

i SEQ ID NO. 14
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22.54%
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                 327 yrAlaGln-----IleCysTyrAsnAsnSerHisAspGlnAsnGlyPheIleValPheG
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                                                                                               292 lyAspMetTyrIleGly-----AsnAspAsnGluArg--
      985 CAGCTGTGGTGCATCTACAGGGC----
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LOCATION: (453<u>1</u>)..(4531)
OTHER INFORMATION: n = a,
FEATURE:
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OTHER INFORMATION: n = a,
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NAME/KEY: misc_feature
LOCATION: (4242)..(4242)
OTHER INFORMATION: n = a
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LOCATION: (4523)..(4523)
OTHER INFORMATION: n = a
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OTHER INFORMATION: n = a
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LOCATION: (4529)..(452)
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US-10-272-411-6
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Matches:
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             ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4545)..(4545)
; OTHER INFORMATION: n equals a, g,
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Matches:
Conservative:
Mismatches:
Indels:
NAME/KEY: misc feature
LOCATION: (4545)..(4545)
OTHER INFORMATION: n = a, t, c or g
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/NM_001399.1
DATABASE BRYRY DATE: 2000-10-31
RELEVANT RESIDUES: (1)..(5307)
PUBLICATION INFORMATION:
DATABASE BACKESSION NUMBER: NCBI/AF040628.1
DATABASE ENTRY DATE: 1998-11-13
RELEVANT RESIDUES: (1)..(5307)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/AF061189.1
DATABASE ENTRY DATE: 1998-11-14
RELEVANT RESIDUES: (1)..(5307)
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APPLICANT: Human Genome Sciences, Inc.

APPLICANT: Human Genome Sciences, Inc.

ITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel.

TITLE OF INVENTION: Human Endokine Alpha
FILE REFERENCE: PF5.1

CURRENT APPLICATION NUMBER: US/10/218,547

CURRENT FILING DATE: 2002-08-15

PRIOR PILING DATE: 2001-08-16

PRIOR PILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin version 3.1

SEQ ID NO 41

LENGTH: 5307
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LOCATION: (4242)...(4242)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (4471)..(447)
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ORGANISM: human
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.093 TTAAGCTACATCCCCGCAGCGGGGGGCTGGAGGTACTGGTGGACGGCACCTACTTCATCT 1152
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                                        925 CCCCTGGCCTCCAGGGACCTTCTGGTGCTGCTGATAAAGCTGGAACTCGAGAAAACCAGC 984
                                                                                                                                                       273 a-AlaHisPheHisLeuSerArgArgArgHisGlnGlySer---MetGlyTyrHisG 292
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| Publication No. US2003010944A1
| GENERAL INFORMATION:
| APPLICANT: Barnes Jewish Hospital
| APPLICANT: Lam, Jonathan
| APPLICANT: Lam, Jonathan
| APPLICANT: Lam, Jonathan
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| APPLICANT: Lam, Jonathan
| FILE REFERENCE: 60019620-0206
| CURRENT FILING DATE: 2001-10-15
| PRIOR FILING DATE: 2001-10-15
| NUMBER OF EXQ ID NOS: 51
| SEQ ID NO 6
| Langthan Applicant Norsion 3.1
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OTHER INFORMATION: n = a,
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LOCATION: (4471)...(4471)
OTHER INFORMATION: n = a,
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NAME/KEY: misc_feature
LOCATION: (4523)..(4523)
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ORGANISM: Homo sapiens
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LOCATION: (4545)..(4545)

COTHER INFORMATION: n equals a, c,

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model
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Run on:

September 15, 2004, 05:12:07; Search time 4190 Seconds (without alignments) 2914.948 Million cell updates/sec US-09-813-329-6 2162 1 MTAETLKPFITPTSANDDGF......DRNAVLREGNNRSYFGIFKV 409 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Title: Perfect score: Sequence: Scoring table:

55026578 Total number of hits satisfying chosen parameters:

27513289 segs, 14931090276 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Command line parameters:
-MODEL=frame+ pln.model -DEV=xlp
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-Copic_1/USPTO_spool_p/US09813329/runat_13092004_102753_21680/app_query.fasta_1.583
-DS=ST -OPMT=fastap -SUFFTX=rst -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-USER=US09813329 @CGN 1 1 6425_@runat_13092004_102753_21680 -NCPU=6 -ICPU=3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

686 bp mRNA linear BST 23-APR-2001	SD13795.5prime SD Drosophila melanogaster Schneider L2 cell culture	CG12919: FBan0012919 located on: 2R 46E1-46E1;: 04/13/2001, mRNA					~		Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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989	rime SD Drosophila	San0012919 located			BG636194.1 GI:13763731		Drosophila melanogaster (fruit fly)	Drosophila melanogaster	Metazoa; Arthropod
BG636194	SD13795.5p	CG12919: FI	sequence.	BG636194	BG636194.1	EST.	Drosophila	Drosophila	Eukaryota,
RESULT 1 BG636194 LOCUS	DEFINITION			ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	

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B1636564 linear EST 10-SEP-2001 SD18286.5prime SD Drosophila melanogaster Schneider L2 cell culture pc72 Drosophila melanogaster cDNA clone SD18286 5 similar to CG12919: FBan0012919 GO:[] located on: 2R 46E1-46E1;: 05/19/2001,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .495
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                                                                                                                                                                                                                                                                           1 (bases 1 to 495)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Leufs, S. and Rubin, G.M.
BDGP/HHMI Droscophila EST Project
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACGACGATGGCGATGGTTCCATTGCGGACGACGAGGACGACGACGACGTTGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                               Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
estimated-cyto:46B13-46E4: 0519/2001
Plate: SD.182 row: H column: 2
Plate: SD.182 row: H column: 2
High quality sequence stop: 491.
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                                                                                                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pOT2; Site 1: EcoR1; Site 2: Xho1; Sfractionated cDNAs were directly ligated into pOT2 Plasmid cDNA library."
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Conservative:
Mismatches:
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BI636564.1 GI:15538774
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99.39%
                                                                                                                    mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 CACCTGAGCAGCAGCAGCGCGCTCACCAAGGAAGTATGGGCTACCATGGAGAATATGTACATA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Bpydroidea; Drosophilidae; Drosophila.
1 (Dases 1 to 686)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DHS-alpha"
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culture_pOT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 GACCAGAACGGATTTATCGTCTTTCAAGAGACACTCCATTCCTGCAGTGCTTGAACAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluArgAsnGluArgIleHisLeuLysAspIleHisAsnAspArgAsnAlaValLeuArg 396
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                                                                                                                                                             Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003831: arm:2R [4876906,5137815]
hit genomic AE003831: arm:2R [4876906,5137815]
estimated-cyto:46B13-46E4: 04/13/2001
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High quality sequence stop: 685.
Location/Qualifiers
1. 686
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                                                                                                                                                                                                                                                                                                                                                                                                             clone="SD13795"
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REFERENCE AUTHORS

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CK135525
RH5169.3prime RH Drosophila melanogaster normalized Head pFIC-1
Drosophila melanogaster CDNA clone RH51659 3 similar to CG12919:
PBan0012919 GO:[] located on: 2R 46E1-46E1; 08/05/2002, mRNA
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One Cyclotron Rd, Berkeley, CA 94720, USA
Eax: 510 486 6798
Email: http://www.fruitfly.org/EsT, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic AE001831: arm:2R [4876906,5137815]
                                                                                                                                                                                          Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Badopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 532)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
Misra, S., Mungall, C.J., Nunoo, J., Parts, N., Li, P., Liao, G.,
Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and
                                                                                                                        328 CTGAAGGACATTCACAACGATCGCAATGCAGTTCTGCGGGGGGGAAACAACCGAAGCTAC 269
                         508 TATTACGTATACGCCCAGATATGCTACAACAACTCGCACGACCAGAACGGATTATCGTC 449
                                                                                              344 PheGlnGlyAspThrProPheLeuGlnCysLeuAsnThrValProThrAsnMetProHis 363
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324 TyrTyrValTyrAlaGlnIleCysTyrAsnAsnSerHisAspGlnAsnGlyPheIleVal

    . 532
    /organism="Drosophila melanogaster"

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Plate: RH.516 row: E column: 11
High quality sequence stop: 382.
Location/Qualitiers
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Other ESTs: RH51659.5prime
Contact: Stapleton, M.
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CKI35525.1 GI:38627461
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic AE003831: arm:2R [4876906,5137815]
estimated-cytc:46B13-46E4: 02/08/2002
Plate: SD-182 row. H column: 2
Plate: SD-181 row. H column: 2
High quality sequence stope: 456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CK135985 508 bp mRNA linear EST 02-DEC-2003 SD18286.3prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster CDNA clone SD18286 3, mRNA sequence.
                                                     365 GAGCAGAATATTCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoda; Arthropoda; Haxapoda; Insecta; Pterygota;
Eukaryota; Metazoda; Arthropoda; Haxapoda; Insecta; Pterygota;
Noppera; Endoprerygoua; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 508)
Harvey,D., Brokatein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Other ESTs: SD18286.Sprime
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/clone_lib="SD Drosophila melanogaster Schneider L2 cell
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                      AsnAlaHisLysLysLysGlnGluArgLysSerArgSerIleAlaAspValArgAsnGlu
                                                                                                                  GluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLysSerSerAsnGluAlaThr
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                   485 CTCCTAGTC 493
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                      200
                                                                                                                  220
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Pred. No.:

FEATURES

549

489

369

at 5'

429

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/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX553466 Glossina morsitans morsitans adult infected gut Glossina morsitans cDNA clone Tse129f05_glc, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 CysLeuAsnThrValProThrAsnMetProHisLysValHisThrCysHisThrSerGly 372
                                                                                                                                                                                                                                                                                                               313 AspGlyValLeuThrValThrAsnThrGlyLeuTyrTyrValTyrAlaGlnIleCysTyr 332
                                                                                                                                                                                                                                                                                                                                                                                     333 AsnAsnSerHisAspGlnAsnGlyPheIleValPheGlnGlyAspThrProPheLeuGln 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota Michaca, Arthropoda, Hexapoda, Insecta, Pterygota, Brachycera, Endopterygota, Diptera, Brachycera, Muscomorpha, Hippoboscoidea, Glossinidae, Glossina.

1 (Dasses 1 to 539)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
                                                                                                                                                                                                                                                                                                                                     373 LeulleHisLeuGluArgAsnGluArgIleHisLeuLysAspIleHisAsnAspArgAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         All clones with suffix glc are reverse primer reads starting end of the cDNA all plc reads are from the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 AlaValLeuArgGluGlyAsnAsnAsnArgSerTyrPheGlyIlePheLyBVal 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 GCGGTCTTGAAGGATTCAAACAATAGAAGTTACTTTGGTTTAATGAAAATC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Thinxton, Cambridge, CB10 18A, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
                                                                                                                                                 612
65
18
14
0
                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
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Genome Biol. 4 (10), R63 (2003)
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Glossina morsitans morsitans
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BX553466.1 GI:33377624
                                                                                                                                              2.99e-25
397.00
85.57%
67.01%
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Best Local Similarity:
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BX553466
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Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads starting at 5'
end of the CDNA all plc reads are from
the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX560278
BX560278 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse49al0_plc, mRNA sequence.
                                                                                                                                                                                                                                        530 TACGTATACGCCCAGATATGCTACAACAACTCGCACGACCAGAACGGATTTATCGTCTTT 471
                                                                                                                                                                                                                                                                                        GlnGlyAspThrProPheLeuGlnCysLeuAsnThrValProThrAsnMetProHisLys 364
                                                                                                                                                                                                                                                                                                               ValHisThrCysHisThrSerGlyLeuIleHisLeuGluArgAsnGluArgIleHisLeu 384
                                                                                                                                                                                                                                                                                                                                                                                                                                      LysAspileHisAsnAspArgAsnAlaValLeuArgCluClyAsnAsnArgSerTyrPhe 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 AAGGACATTCACAACGATGCAGTTCTGCGGGAGGGAAACAACCGAAGCTACTTT 291
                                                                                                                                                                                                                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune
                                                                                                                                                                                                                    TyrValTyrAlaGlnIleCysTyrAsnAsnSerHisAspGlnAsnGlyPheIleValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidea; Glossinidae; Glossina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Glossina morsitans morsitans"
                                                     532
83
0
0
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                                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                             Indels:
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/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse49a10_plc"
                                                                                                                                               Gaps:
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Genome Biol. 4 (10), R63 (2003)
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BX560278.1 GI:33368472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 GGCATCTTCAAGGTG 276
                                                   1.7e-31
466.00
100.00%
97.65%
21.55%
                                                                                       Percent Similarity:
Best Local Similarity:
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                                   Alignment Scores:
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Tiger Shrimp

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/dev_stage="Mature broodstock"
/clone_lib="Giant tiger prawn eyestalk cDNA library"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
Xho! mRNA isolated from total eyestalk tissue and used to
construct directional cDNA library in Lambda ZAP Express.
Clones excised in vivo to create phagemids in pBK-CMV for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nlleCysTyrAsnAsnSerHisAspGlnAsnGlyPhelleValPheGlnGlyAspThrPr 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnGluLysSerSerAsnGluAlaThrSerLysGluSerProAlaProLeuHisHisArg 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 ArgargMetHisSerArgHisArgHisLeuLeuValArgLysAlaArgSerGluAspSer 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 yTyrHisGlyAspMetTyrIleGlyAsnAspAsnGluArgAsnSerTyrGlnGlyHisPh 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ceracacidecida en contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contra contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----CGCCCACACGAGGAGTTAGCGAAGA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGAAGATCCCGAGGAAGAAGCAGAGTCA----ACGCCGGCGCGCG-----CACCAA 92
  Bumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
                                                                                                                                                                                                                         Australian Institute of Maxine Science
PMB 3 Townsville Mail Centre, Townsville QLD 4810, Australia
Fal: +61 7 4723 4444
Fax: +61 7 4772 5852
Email: kwilson@aims.gov.au
No significant database matches when searched using a filter to
remove low-comploatity sequence, September 3 1998. When searched
with the filter turned off, shows homology to large proline-rich
protein bat2 from humans (p= 2.0e-07)
Insert Length: 1000 Std Error: 100.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eGlnThrArgAspGlyValLeuThrValThrAsnThrGlyLeuTyrTyrValTyrAlaGl
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                                                                          Moore, S.S.
from the B
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26
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8
                       Penaeidae; Penaeus.

1 (bases I to $26)

1 Lehnert,S.A. Wilson,K.J., Byrne,K. and Moc
Tissue-Specific Expressed Sequence Tags from Penaeus monodon

Mar. Biotechnol. 1 (5), 465-476 (1999)

Contact: Wilson Kate J

Marine Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Penaeus monodon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Eyestalk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:6687"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-813-329-6 (1-409) x AI253821 (1-526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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193.50
46.96%
32.60%
8.95%
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Query Match:
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                                                  REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                    /note="country: Zimbabwe; EST from adult gut infected with T.brucei"
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                                                                       /db xref="taxon:37546"
/clone="Teel29f05 glc"
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGGCAATIGITITIGACTITIGIA-------CICTIGGGTIGCICG
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AIMS-P.mon24 Giant tiger prawn eyestalk cDNA library Penaeus
monodon cDNA 5', mRNA sequence.
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organism="Glossina morsitans morsitans"
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Conservative:
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Penaeus monodon
                             /mol_type="mRNA"
/sub_species="morsitans"
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Library Submitted (108-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web : Web : Web : Web : Reader of this GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzil; Zygosaccharomyces rouxii, Saccharomyces servazzil; Zygosaccharomyces rouxii, Saccharomyces kluyveron, Web : Randomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta. Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to keywords for description of this sequence and for the sequence of the other extremity of this insert.
                                                                                                                                                                                                                                                                                      Candida tropicalis
Candida tropicalis
Candida tropicalis
Candida tropicalis
Candida tropicalis
Candida tropicalis
Bustryota, Fungi; Ascomycota; Saccharomycetales; Candida.
Saccharomycetales; mitosporic Saccharomycetales; Candida.

I (bases 1 to 917)
S Soudit. J.L., Aigle, M., Artiguenave, F., Blandin. G.,
Ge-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies

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Blandin,G., Ozier-Kalogeropoulos,O., Wincker,P., Artiguenave,F. and
                                                                                                                                 CNSO7DXT
T3 end of clone BD0AA016E09 of library BD0AA from strain CBS 94 of Candida tropicalis, genomic survey sequence.
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/note="similar to Saccharomyces cerevisiae ORF YKL088w
similarity to C.tropicalis hal3 protein, to C-term. of
Sis2p and to hypothetical protein YOR054c ]
1 putative frameshift(s)"
/evidence=not_experimental
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62
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/mol_type="genomic DNA"
/strain="CBS 94"
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/clone="BD0AA016E09"
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/note="end : T3"
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116 Asp
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AL108596. AL108596. I GI:5628900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqrefégenoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                            CACCGGGGGCCCACCTACCTTCCCAGGAACGCTGCCGTCTACATCCGGGACCTGGACCA 458
                                                                                                                           PheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLysValAspGlyLeuThr 115
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sThrSerGlyLeuIleHisLeuGluArgAsnGluArgIleHisLeuLysAspIleHisAs 389
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                                                                                               389 nAspArgAsnAlaValLeuArgGluGlyAsnAsnArgSerTyrPheGlyIlePheLysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Mismatches:
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/clone="BACN37D20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="DrosBAC"
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/dev_stage="adult"
//dev_stage="adult"
/lab_host="bH10B"
/clone_lib="CSEQCHN74"
/clone_lib="CSEQCHN74"
/notoe="Organ: kidney + adrenal; Vector: pBluescript II
/note="Organ: kidney + adrenal; Vector: pBluescript II
/note="Organ: kidney + adrenal; Vector: pBluescript II
/note="Organ: kidney + adrenal; Vector: pBluescript II
/note="Organ: kidney + adrenal prepared clones.

CDNA synthesis was initiated using an oligo(dT) primer,

using methylated C in the first strand prediction.

Following this first strand reaction, double-stranded cDNA
was blunted, ligated to Not! adapters, digested with
Compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., pNAS
(1994) 91: 9228-9212 and Bonaldo et al., Genome Research 6
(1995): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 Gludrg------AsnSerTyrGlnGlyHisPheGlnThrArgAspGlyValLeuThr 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 GCCAGGCAGAAGATTGCTGTGAAAATGGTCCACGCTGACATCTCC-----ATCAACATG 541
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                              /mol_type="mRNA"
/strain="Compton Line 151"
                                                                                                                                                         organism="Gallus gallus"
                                        PO Box 88, Manchester, M60 10D, U
121: 01612008930
Fax: 01612160409
Email: Simon.Hubbard@umist.ac.uk.
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Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                              338
                                                                                                                                                                                                                                           396 AGGTTATTAGATGAA---GAAGAAGATTG-----AATGAAGAGGACGAAGAAGATGAG 446
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                                                                                                                                                                                                                                                                                                                                                                                                               447 GATGAAGAAGAGGGTGATGACGGC-------GAAGAAGATGGTGATGCG 488
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                     40 LeuValLeuGlyPheileGlyLeuGlyLeuValValAlaileLeuAlaLeuThrileTrp
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Contact: Simon Hubbard
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CD851068 746 bp mRNA linear EST 11-JUL-2003 DH0AL5ZH01ZM1 HaDevR5 Helianthus annuus CDNA clone HaDevR55H01,
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                                                                                                                                                                                                                                                                                      468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Genoplante Genoplante Genoplante Genoplante Genoplante 93, rue Henri Rochefort 91025 EVRY CEDEX France 93, rue Henri Rochefort 91025 EVRY CEDEX France Fax: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Finis sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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                                                                                                          289 TCACCTGGTGCCTGATCATTTTTTACCAATGACGCCCTGGATGCCACTCTCGTCTCCTG
                                                                                                                                                       301 -GluArgAsnSerTyrGlnGlyHis---PheGlnThrArgAspGlyValLeuThrValTh
                                                                                                                                                                                                                                                                                  409 GAATTCTGGGATATATTCAGTATACAGCCAGGTTCTGTACAACGATTCCAGGTTCACGAT
                                                                                                                                                                                                                                                                                                                            339 nGlyPhelleValPheGln-------GlyAspThrProPheLeuGl
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/tissue_type="4 days after self-pollination embryo"
/clone_lib="HaDevR5"
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                                                                     291 -His-----GlyAspMetTyrIleGlyAsnAspAsn---
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/cultivar="psc8"
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CD851068.1 GI:32534884
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/clone lib="NICHD_XGC_SwblN"
/clone lib="NICHD_XGC_SwblN"
/clone lib="NICHD_XGC_SwblN"
/clone lib="NICHD_XGC_SwblN"
/note="Vector: pExpress-1; Site_1: EcoRV; Site_2: NotI;
Bulk tissue was collected from a whole 10 month old male
from the F6 strain. 1st strand cDNA was primed with a Not
I - oligo(dT) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pExpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cot5 with a
180-fold reduction of actin. A non-normalized version of
this library is also available (NICHD XGC_Swbl). Library
was constructed by Open Biosystems (Huntsville, AL)."
                                                                                    CF590046 965 bp mRNA linear EST 26-SEP-2003
AGENCOURT_15681475 NICHD_XGC_SwblN Silurana tropicalis cDNA clone
                                                                                                                                                                                                                                                                                        Ampliance, Silurana.

Kenopodinae; Silurana.

I (bases 1 to 965)

S MIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: capaba-remail.nih.gov

Tissue Procurement: Rob Granger, University of Virginia

CDNA Library Preparation: Open Biosystems

CDNA Library Prayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be the p://inage:llnl.gov

Plate: LLAM14744 row: g column: 24

High quality sequence start: 23

High quality sequence start: 23

High quality sequence start: 23

High quality sequence start: 23

High quality sequence start: 23
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                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 GluLysSerSerAsnGluAlaThrSerLysGluSerProAlaProLeuHisHisArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 ArgMetHisSerArgHisArgHisLeuLeuValArgLysAlaArgSerGluAspSerArg
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33
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AGCAAGCACACATTTCTTTGGGGCCATCCGCCTA 577
                                                                                                                                                                                                               Silurana tropicalis (western clawed frog)
Silurana tropicalis
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/organism="Silurana tropicalis"
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                                                                                                                      IMAGE: 7020818 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7020818"
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Schistosoma japonicum
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Schistosoma japonicum
Sukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeldida; Schistosomatoidea; Schistosoma.

1 (bases 1 to 724)
Hu, W., Yan, Q., Shen, D.K., Liu, F., Zhu, Z.D., Song, H.D., Xu, X.R., Wang, Z.J., Rong, Y.P., Zeng, L.C., Wu, J., Zhang, X., Wang, J.J.,
Wang, Z.Y., Fu, G., Zhang, X.L., Wang, Z.Q., Brindley, P.J., McManus, D.P., Xue, C.L., Feng, Z., Chen, Z. and Han, Z.G.
Evolutionary and biomedical implications of a Schistosoma japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 23-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 CATTACAATGACGATCACGATGAAATTGGATTTCATCTTCAAGTGAACAATCAACCTATT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 LeuGlnCysLeuAsnThrValProThrAsnMetProHisLysValHisThrCysHisThr 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 GCTCAAGTGACACTTCTTAGAAAGAAGGAAGACGTTTTAGTTTTCAAGGAGGCTAGCTCACCG 292
                                                                                                                                                                                                                                                                                                                              /clone libe Rea Brain Normalized Library, BB16"
/notes Organ: brain; Vector: pT73-Pac; Site 1: EcoR1;
Site 2: Not1; The BB16 library was contributed by the
Soare laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6 (9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups."
                                                                                                                                              European bees, predominantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 ArgAsnAlaValLeuArgGluGlyAsnAsnArgSerTyrPheGlyIlePheLysVal 409
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32
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17
                                                                                                                                                                                                                                                              /tissue_type="brain"
/dev_stage="adult_worker_honey_bee"
/lab_host="DH108"
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Matches:
Conservative:
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primer: AGCGGATAACAATTTCACACAGGA
                                                                                              'organism="Apis mellifera"
                                                                                                                     /mol_type="mRNA"
/strain="mixed strains of
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Nat. Genet. 35 (2), 139-147 (2003)
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Seq primer: Accessions.
High quality sequence stop: 550.
Location/Qualifiers
                                                                                                                                                                                                                   /clone="BB160016A20A06"
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This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
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BB160016A20A06.5 Bee Brain Normalized Library, BB16 Apis mellifera
CDNA clone BB160016A20A06 5', mRNA sequence.
B1514804
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Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
Amotians, J., Robertson, H.M., Soares, B. and Robinson, G.E.
Annotated expressed sequence tags and cDNA microarrays for studies
of brain and behavior in the honey bee
                                                                                                                                                                                                            134 AspAspAspValSerTyrSerSerValAspAspValGlyAlaAspTyrGluAspTyrThr 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GAGGGGGAGGTGATGATGATGTCAGCATTGGTGATGCAGAAGACGGAAGTGATGAC 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspGluPheGlnLysGluTyrGluAsnAlaLeuIleAspTyrProLysLysValAspGly 113
                                                                                                                                                                                                                                                                                                             154 AspMetLeuAsnLysLeuAsnAsnAlaHisThrGlyThrThrProThrSerGluThrThr 173
                                                                                                                                                                                                                                                                                                                                                            ------CCGGCAGATGTTTCAGAAGATGAT 353
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                   GATGAAAGTGATGAAGAAATTGACGCCATATTGGAT-------TCCACGAACCCT
                                                                                                                  114 LeuThrAspGluGluAspAspAspAspGlyAspGlyLeuAspSerileAlaAspAspGlu
                                                                                                                                                               222 GCTCTGGATGCTGACGCTGATTATGATTACGATAATCTGGACGAAATCGCTGACGAC
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282 GATGATGATTTGGTGGGTAATGCTAGTGATGAAGGAATGGAGTTT-------
                                                                                                                                                                                                                                                                                                                                                                                                         174 AlaGluGlyGluGlyGluThrAsp-----SerAlaSerSerAlaSerAsnAsp
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Tel: 217 265 0309
Fax: 217 244 3499
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Plate: BB160016A20 row: A column: 06
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570 AAGAAGGCTAAAAAGTCCCAAATCTAAAAAG 599
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Department of Entomology
University of Illinois
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112

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Schistosoma japonicum
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThraspGluGluAspAspAspAspGlyAspGlyLeuAspSerIleAlaAspAspGluAsp 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspValArgAsnGluGluGlnAsnIleGlnGlyAsnHisThrGluLeuGlnGluLysSer 234
           Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 CTTAGTAACCATGACTCGTCCGATTCTGGTAACAATAATGCTACCAGGACATGATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 AspPheThrSerTyrAsnAlaHisLysLysLysGlnGluArgLysSerArgSerIleAla
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45
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79
52
                                                                                                                                 organism="Schistosoma japonicum"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                           (1-724)
                                                                                        Email: hanzg@chgc.sh.cn.
Location/Qualifiers
                                                                                                                                                                         sex="female"
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linear EST 23-OCT-2003 mRNA sequence.

BU803616 732 bp mRNA 225AFWEDS SJF Schistosoma japonicum cDNA, BU803616 GI:28360623

DEFINITION ACCESSION VERSION KEYWORDS

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1 (bases I to 732)
Hu, W., Yan, Q., Shen, D.K., Liu, F., Zhu, Z.D., Song, H.D., Xu, X.R.,
Wang, Z.J., Rong, Y.P., Zeng, L.C., Wu, J., Zhang, X., Wang, J.J.,
Xu, X.N., Wang, Y.P., Fu, G., Zhang, X.L., Wang, J. Z.O., Brindley, P.J.,
McManus, D.P., Xue, C.L., Feng, Z., Chen, Z. and Han, Z.G.
Evolutionary and biomedical implications of a Schistosoma japonicum
complementary DNA resource
Nat. Genet. 35 (2), 139-147 (2003)
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                                                                                                                                                                                                                                                                                                             Contact: Zeguang Han
Contact: Zeguang Han
Contact: Astional Human Genome Center at Shanghai
151 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
161 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 AATAAAAATCTCGAAGTCGTAGTCCCATCGTCTTCCTCGGACTCAGACTCTGGATTCTTCC
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Schistosoma japonicum
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
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Matches:
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Mismatches:
Indels:
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